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Gencore version 4.5									
protein - protein search, using sw model									
run on: September 13, 2002, 12:05:54 ; Search time 13.54 Seconds									
{without alignments} 1286.839 Million cell updates/sec									
title: US-09-471-459A-5	score: 24.08	sequence: 1 MSCLMVERGEILFENPDON.....	length: 1	DB: PDHDHAGQSTEEQEGDSP	seq: 450	gapext: 0.5	gapop: 10.0	gapext: 0.5	gapop: 10.0
core table: BLOSUM62	searched: 105224 seqs, 3819550 residues	total number of hits satisfying chosen parameters: 105224	minimum DB seq length: 0	maximum DB seq length: 200000000	cost-processing: Minimum Match 0%	Maximum Match 10%	Listing first 45 summaries		
database : SwissProt_40:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								
SUMMARIES									
result No.	Score	Match	Length	DB	ID	Description	RESULT ID	CN7B_HUMAN	STANDARD; PRT; 450 AA.
1	24.08	100.0	450	1	CN7B_HUMAN	Q9np56 homo sapien	CN7B_HUMAN	CN7B_HUMAN	
2	21.92	91.0	446	1	CNTB_MOUSE	Q9qkq1 mus musculus	CNTB_MOUSE	CNTB_MOUSE	
3	14.25	59.2	456	1	CNTA_MOUSE	P70453 mus musculus	CNTA_MOUSE	CNTA_MOUSE	
4	1419.5	58.9	482	1	CNTA_HUMAN	Q13946 homo sapien	CNTA_HUMAN	CNTA_HUMAN	
5	1397.5	58.0	426	1	CNTA_RAT	Q08533 rattus norvegicus	CNTA_RAT	CNTA_RAT	
6	604.5	25.1	809	1	CN4D_HUMAN	Q00459 homo sapien	CN4D_HUMAN	CN4D_HUMAN	
7	603.5	25.1	672	1	CN4D_RAT	P14270 rattus norvegicus	CN4D_RAT	CN4D_RAT	
8	580.5	24.1	721	1	CN4B_RAT	P14646 rattus norvegicus	CN4B_RAT	CN4B_RAT	
9	567.6	23.6	736	1	CN4B_HUMAN	Q07743 homo sapien	CN4B_HUMAN	CN4B_HUMAN	
10	555.5	23.5	886	1	CN4A_HUMAN	P27815 homo sapien	CN4A_HUMAN	CN4A_HUMAN	
11	559.5	23.2	610	1	CN4Z_RAT	P14645 rattus norvegicus	CN4Z_RAT	CN4Z_RAT	
12	559.5	23.2	844	1	CN4A_RAT	P54748 rattus norvegicus	CN4A_RAT	CN4A_RAT	
13	553	23.0	712	1	CN4C_HUMAN	Q08493 homo sapien	CN4C_HUMAN	CN4C_HUMAN	
14	529.5	22.0	536	1	CN4C_RAT	P14644 rattus norvegicus	CN4C_RAT	CN4C_RAT	
15	517.1	21.5	549	1	YST1_CAEEL	Q22000 coenorhabditis elegans	YST1_CAEEL	YST1_CAEEL	
16	493	20.5	584	1	CNAL_DROME	P12252 drosophila melanogaster	CNAL_DROME	CNAL_DROME	
17	468	19.4	535	1	CNIB_MOUSE	Q01065 mus musculus	CNIB_MOUSE	CNIB_MOUSE	
18	467	19.4	534	1	CNIB_BOVIN	Q01061 bos taurus	CNIB_BOVIN	CNIB_BOVIN	
19	466	19.4	534	1	CN1A_HUMAN	P54750 homo sapien	CN1A_HUMAN	CN1A_HUMAN	
20	466	19.4	535	1	CN1B_RAT	Q01066 rattus norvegicus	CN1B_RAT	CN1B_RAT	
21	466	19.4	565	1	CN1A_MOUSE	Q01481 mus musculus	CN1A_MOUSE	CN1A_MOUSE	
22	461	19.1	664	1	YFGK_CAEEL	Q18596 caenorhabditis elegans	YFGK_CAEEL	YFGK_CAEEL	
23	461	19.1	793	1	REGA_DICTI	Q23917 dictyostelia regens	REGA_DICTI	REGA_DICTI	
24	456	19.1	823	1	CN8A_MOUSE	Q88502 mus musculus	CN8A_MOUSE	CN8A_MOUSE	
25	454.5	18.9	529	1	CN1A_BOVIN	P14100 bos taurus	CN1A_BOVIN	CN1A_BOVIN	
26	452.5	18.8	768	1	CN1C_RAT	Q63421 rattus norvegicus	CN1C_RAT	CN1C_RAT	
27	450.5	18.7	654	1	CN1C_MOUSE	Q64338 mus musculus	CN1C_MOUSE	CN1C_MOUSE	
28	449	18.6	536	1	CN1B_HUMAN	Q01064 homo sapien	CN1B_HUMAN	CN1B_HUMAN	
29	448.5	18.6	709	1	CN1C_HUMAN	Q14123 homo sapien	CN1C_HUMAN	CN1C_HUMAN	
30	445.5	18.5	713	1	CN8A_HUMAN	Q06058 homo sapien	CN8A_HUMAN	CN8A_HUMAN	
31	441	18.3	539	1	CN8B_HUMAN	Q95263 homo sapien	CN8B_HUMAN	CN8B_HUMAN	
32	422	17.5	534	1	CN9A_MOUSE	Q70628 mus musculus	CN9A_MOUSE	CN9A_MOUSE	
33	399	16.6	593	1	CN9A_HUMAN	Q76083 homo sapien	CN9A_HUMAN	CN9A_HUMAN	

DR Pfam; PF00233; PDEase; 1.  
 DR PRINTS; PR00387; PDESTERASE1.  
 DR SMART; SM00471; HDC\_1.  
 DR PROSITE; PS0016; PDEASE\_I; 1.  
 KW Hydrolase; CAMP.  
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).  
 SQ 450 AA: 51835 MW: EC142BB3E2BL0028 CRC64;

Query Match 100.0%; Score 2408; DB 1; Length 450;  
 Best Local Similarity 100.0%; Pred. No. 9. 6e-18; Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSCIMVRCCGETLFENDONAKCVCMLGDIRLRLQGTYAERRGSYPPIDFLNSTYS 60  
 1 MSCIMVRCCGETLFENDONAKCVCMLGDIRLRLQGTYAERRGSYPPIDFLNSTYS 60

QY 61 GEIGTKKKVKKRLLSFRYHSLRJGTPQAPHLILDEDYLGQARHMLSKVGMMDEF 120  
 61 GEIGTKKKVKKRLLSFRYHSLRJGTPQAPHLILDEDYLGQARHMLSKVGMMDEF 120

Db 121 LFDRLTNGNSLVTLCHFNLNTHGLIHLHFKLMDVTHRLWYQDHSQNYHNAHAAD 180  
 121 LFDRLTNGNSLVTLCHFNLNTHGLIHLHFKLMDVTHRLWYQDHSQNYHNAHAAD 180

QY 181 VTOAMHCYLYKEPKLASFPLDMLGLAALAAHVDHPGVNOPLFLKTNNHILANLYNMS 240  
 181 VTOAMHCYLYKEPKLASFPLDMLGLAALAAHVDHPGVNOPLFLKTNNHILANLYNMS 240

Db 241 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300  
 241 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300

QY 301 KDLRLDAQHFMQIAKCADCNPCTIWIENSKWNSKSERVEEFYFQGELEQKELEIS 360  
 301 KDLRLDAQHFMQIAKCADCNPCTIWIENSKWNSKSERVEEFYFQGELEQKELEIS 360

Db 361 PLCNOQDKSITPSIOLGFMSYIVEPLFREWAHFGNSTISENMGLHLANKWKSLLPRO 420  
 361 PLCNOQDKSITPSIOLGFMSYIVEPLFREWAHFGNSTISENMGLHLANKWKSLLPRO 420

QY 421 HRSRGSSGSPDHADQGQSTESERQEGDSP 450  
 421 HRSRGSSGSPDHADQGQSTESERQEGDSP 450

Db 421 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300  
 421 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300

RESULT 2

CNTB\_MOUSE STANDARD: PRT; 446 AA.

09QX01; 16-OCT-2001 (Rel. 40, created)  
 16-OCT-2001 (Rel. 40, last sequence update)  
 16-OCT-2001 (Rel. 40, last annotation update) 7B (EC 3.1.4.17).  
 DE CAMP-specific 3',5'-cyclic phosphodiesterase

GN PDE7B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 [1] SEQUENCE FROM N.A.

RP MEDLINE=2008773; PubMed=10638442;  
 RA Hetman J.M.; Soderling S.H.; Glavas N.A.; Beavo J.A.;  
 RT Cloning and characterization of PDE7B, a CAMP-specific  
 phosphodiesterase.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476 (2000).  
 RN [2] SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;  
 RX MEDLINE=20329226; PubMed=10872823;  
 RA Gardner C.E.; Robas N.M.; Cowell D.; Fidock M.D.;  
 RT "Cloning and characterization of the human and mouse PDE7B, a novel  
 CAMP-specific nucleotide phosphodiesterase.";

RL Biochem. Biophys. Res. Commun. 272:186-192(2000).  
 DR -!- FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL  
 CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.  
 DR -!- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =  
 CC ADENOSINE 5'-PHOSPHATE.  
 DR -!- COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).  
 CC -!- ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.  
 CC -!- INSENSITIVE TO ZARRINAST, ROLFERM, AND MILRINONE.  
 CC -!- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.  
 CC -!- DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO  
 CC -!- PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
 CC FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to license@ib-sib.ch).  
 DR EMBL; AF19039; AF25195; 1.  
 DR EMBL; AU25159; CAB9530; 1.  
 DR EMBL; MGJ:132752; PdB; 1.  
 DR MGD; MGJ:132752; PdB; 1.  
 DR InterPro; IPR00367; PDEase.  
 DR InterPro; IPR00373; PDEase.  
 DR PRINTS; PR00387; PDESTERASE1.  
 DR SMART; SM00471; HDC\_1.  
 DR PROSITE; PS0016; PDEASE\_I; 1.  
 KW Hydrolase; CAMP.  
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).  
 SQ 446 AA: 51337 MW: 7C052664B693A5A8 CRC64;

Query Match 91.0%; Score 2192; DB 1; Length 446;  
 Best Local Similarity 91.6%; Pred. No. 3e-170; Matches 413; Conservative 13; Mismatches 30; Indels 6; Gaps 2;

QY 1 MSCIMVRCCGETLFENDONAKCVCMLGDIRLRLQGTYAERRGSYPPIDFLNSTYS 60  
 1 MSCIMVRCCGETLFENDONAKCVCMLGDIRLRLQGTYAERRGSYPPIDFLNSTYS 60

QY 61 GEIGTKKKVKKRLLSFRYHSLRJGTPQAPHLILDEDYLGQARHMLSKVGMMDEF 120  
 61 GEIGTKKKVKKRLLSFRYHSLRJGTPQAPHLILDEDYLGQARHMLSKVGMMDEF 120

Db 121 LFDRLTNGNSLVTLCHFNLNTHGLIHLHFKLMDVTHRLWYQDHSQNYHNAHAAD 180  
 121 LFDRLTNGNSLVTLCHFNLNTHGLIHLHFKLMDVTHRLWYQDHSQNYHNAHAAD 180

QY 181 VTOAMHCYLYKEPKLASFPLDMLGLAALAAHVDHPGVNOPLFLKTNNHILANLYNMS 240  
 181 VTOAMHCYLYKEPKLASFPLDMLGLAALAAHVDHPGVNOPLFLKTNNHILANLYNMS 240

Db 241 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300  
 241 VLENHHWRSTIGMRLRSRLLAHPLKEMTODIEQQLGSLILATDINRONEFLTRKALHN 300

QY 301 KDLRLDAQHFMQIAKCADCNPCTIWIENSKWNSKSERVEEFYFQGELEQKELEIS 360  
 301 KDLRLDAQHFMQIAKCADCNPCTIWIENSKWNSKSERVEEFYFQGELEQKELEIS 360

Db 361 PLCNOQDKSITPSIOLGFMSYIVEPLFREWAHFGNSTISENMGLHLANKWKSLLPRO 420  
 361 PLCNOQDKSITPSIOLGFMSYIVEPLFREWAHFGNSTISENMGLHLANKWKSLLPRO 420

QY 421 HRSRGSSGSPDHADQGQSTESERQEGDSP 450  
 421 HRSRGSSGSPDHADQGQSTESERQEGDSP 450

Db 421 HRRRGSG----QDLAGPAPETLEQEGATP 446







RESULT 7

CH4D\_RAT STANDARD; PRT; 672 AA.

ID CN4D\_RAT

AC P14270; CC 01-JAN-1990 (Rel. 13, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CAMP-dependent 3', 5'-cyclic phosphodiesterase 4D (EC 3.1.4.17)

DE (PDE4D).

GN PDE4D.

OS Rattus norvegicus (Rat).

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBL\_Taxid:10116;

RN [1] SEQUENCE FROM N.A. (FORMS PDE3.1; PDE3.2, AND PDE3.3).

RX MEDLINE=9308055; PUBMED=803568;

RA Sette C., Vicini E., Conti M.;

RT "The ratPDE3/IVD differentially activated by cAMP-dependent protein kinase."; J. Biol. Chem. 269:18271-18274(1994).

RA Conti M.;

RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.

RN [3] SEQUENCE OF 95-672 FROM N.A. (FORM PDE3.3).

RX MEDLINE=95047442; PUBMED=7956996;

RA Bolger G.B., Rodgers L., Riggs M.;

RT "Differential CNS expression of alternative mRNA isoforms of the mammalian genes encoding cAMP-specific phosphodiesterases."; Gene 149:237-244(1994).

RN [4] SEQUENCE FROM N.A. (FORMS PDE3.1 AND PDE3.2).

RC STRAIN=WISTAR;

RX MEDLINE=94103244; PUBMED=8276818;

RA Monaco L., Vicini E., Conti M.;

RT "Structure of two rat genes coding for closely related rat cAMP-sensitive cAMP phosphodiesterases. Multiple mRNA variants originate from alternative splicing and multiple start sites."; J. Biol. Chem. 269:347-357(1994).

RN [5] SEQUENCE FROM N.A. (FORM PDE3.1).

RC TISSUE=TESTIS;

RX MEDLINE=90046763; PUBMED=2554303;

RA Swinnen J.V., Joseph D.R., Conti M.;

RT "The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormones and cAMP"; PROC. NATL. ACAD. SCI. U.S.A. 86:8197-8201(1989).

RN [7] SEQUENCE OF 234-672 FROM N.A.

RC TISSUE=TESTIS;

RX MEDLINE=83315990; PUBMED=2546153;

RA Swinnen J.V., Joseph D.R., Conti M.;

Db 530 VLENHHLAVGFKLLOEENGDIQFOLTTKKORRSLRKMYVIDIVATDKSKHMLLADLKTIV 589

QY 299 HNKD----LRLEDQDRHFMQLQALKCADICNPICRIMSKQSRVCEFFYRGELE 352

590 ETKKVNTSSGVLILDKYSDR1QVLONMVHCAQDLSNPTKPLQLYRQWTDRIMPFRRGDR 649

QY 353 QKFEFLFISPICNQDKSTISIOLQFMSVYVEPFLRFENAHFGNSTISENMIGHTAINKAQ 412

650 RERGMELISPACDKHNAVSVERKSQVGFIDTIVHPLWETWADLHFD-AQDIDLTLEDNREW 707

QY 413 WKLSPLRQHNSRGSSGGDHDHAGQTE-----EQRGDS 449

708 YOSTIPQ-----SPSPADDPERGQDTEKFOELTLEEDGES 746

RT "Molecular cloning of rat homologues of the *Drosophila melanogaster* duncane cAMP phosphodiesterase: evidence for a family of genes."; PROC. NATL. ACAD. SCI. U.S.A. 86:5325-5329(1989).

CC -!- CATALYTIC ACTIVITY: ADENOSINE 3', 5'-CYCLIC PHOSPHATE + H(2)O = ADENOSINE 5'-PHOSPHATE.

CC -!- ENZYME REGULATION: INHIBITED BY ROLIPRAM.

CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -!- PTM: FORM PDE3.3 IS RAPIDLY ACTIVATED BY PKA THROUGH PHOSPHORYLATION.

CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.

CC -!- FAMILY

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CC -!- DR EMBL: U09457; AAAB1869\_1; -.

CC -!- DR EMBL: U09456; AAAC2093\_1; -.

CC -!- DR EMBL: L27059; AAAB3685\_1; -.

CC -!- DR EMBL: U01280; AAAB1892\_1; -.

CC -!- DR EMBL: U01278; AAAB1892\_1; -.

CC -!- DR EMBL: U01282; AAAB1892\_1; -.

CC -!- DR EMBL: U01284; AAAB1892\_1; -.

CC -!- DR EMBL: U01285; AAAB1892\_1; -.

CC -!- DR EMBL: U01286; AAAB1892\_1; -.

CC -!- DR EMBL: U01287; AAAB1892\_1; -.

CC -!- DR EMBL: U01288; AAAB1892\_1; -.

CC -!- DR EMBL: U01289; AAAB1892\_1; -.

CC -!- DR EMBL: U01290; AAAB1892\_1; -.

CC -!- DR EMBL: U01291; AAAB1892\_1; -.

CC -!- DR EMBL: U01292; AAAB1892\_1; -.

CC -!- DR EMBL: U01293; AAAB1892\_1; -.

CC -!- DR EMBL: U01294; AAAB1892\_1; -.

CC -!- DR EMBL: U01295; AAAB1892\_1; -.

CC -!- DR EMBL: U01296; AAAB1892\_1; -.

CC -!- DR EMBL: U01297; AAAB1892\_1; -.

CC -!- DR EMBL: U01298; AAAB1892\_1; -.

CC -!- DR EMBL: U01299; AAAB1892\_1; -.

CC -!- DR EMBL: U01283; AAAB1892\_1; -.

CC -!- DR EMBL: U01284; AAAB1892\_1; -.

CC -!- DR EMBL: U01285; AAAB1892\_1; -.

CC -!- DR EMBL: U01286; AAAB1892\_1; -.

CC -!- DR EMBL: U01287; AAAB1892\_1; -.

CC -!- DR EMBL: U01279; AAAB1892\_1; -.

CC -!- DR EMBL: U009455; AAAC2040\_1; -.

CC -!- DR EMBL: L27060; AAC26969\_1; -.

CC -!- DR PIR: A34414; A34414.

CC -!- DR PIR: C33904; C33904.

CC -!- DR InterPro: IPI003607; H2C.

CC -!- DR InterPro: IPI002073; PDEase.

CC -!- DR Pfam: PF00233; PDBase\_1.

CC -!- DR PIR: PR00387; PDESTERASE.

CC -!- DR SMART: SM00171; Hdc\_1.

CC -!- DR PROSITE: PS00126; PDEASE\_1; -.

CC -!- DR KW Hydrolase; cAMP; Alternative splicing; Multigene family; Phosphorylation.

CC -!- FT VASPLIC 1 133 MHVNPFPFRHWSICFDVONGTSGRSPLDPMTSPGSLI LQANFHNSQRESEYFLRSYDSDPSKPSRNSSIASDING DDLVTFQAYLQASIGVNRNFAANTLNQDRPSKRSPCM OQSPNKKATV->MKEQPCAGIUGYGMGKAPPAL GGRVKRURTERSPPLFLA (IN ISOFORM PDE3.1).

CC -!- FT VASPLIC 1 167 MISSING (IN ISOFORM PDE3.2).

CC -!- FT CONFLICT 95 A->N (IN REF. 3).

CC -!- FT CONFLICT 95 MISSING (IN REF. 4).

CC -!- FT CONFLICT 349 G->E (IN REF. 3).

CC -!- FT CONFLICT 510 G->E (IN REF. 3).

CC -!- FT CONFLICT 626 C->Y (IN REF. 3).

CC -!- SQ SEQUENCE 672 AA; 76263 MW; 63CE38FA654ABDD CRC64;

Query Match 25.1%; Score 603.5; DB 1; Length 672;

Best Local Similarity 33.3%; Pre. 2.9e-41;

Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;

QY 66 KKKVKRLIS---FORYFHASRLRGTIPQAPLHILDEDYLQGARHMLSKVGMWDFDFI 121





DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CAMP-dependent 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17)  
DE (PDE42) (PDE46).  
GN PDE4A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
NCBI-TAXID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (PDE4A RD1).  
RX MEDLINE=94019330; PubMed=8413254;  
RX MEDLINE=94019330; PubMed=8413254;  
RX MEDLINE=93343959; PubMed=9677330;  
RA Sullivan M., Rena G., Beeg F., Gordon L., Olsen A. S., Houslay M.D.;  
RT "Identification and characterization of the human homologue of the  
short PDE4A cAMP-specific phosphodiesterase RD1 (PDE4A1) by analysis  
of the human HsPDE4A gene locus located at chromosome 19p13.2.";  
RL Biochem. J. 333:693-703(1998).  
RN [3]  
RP SEQUENCE OF 112-886 FROM N.A.  
RC TISSUE=Monocytes;  
RX MEDLINE=90258824; PubMed=2160382;  
RA Livi G., Kmetz P., McHale M.M., Cieslinski L.B., Sathe G.M.,  
RT Taylor D.P., Davis R.L., Torphy T.J., Balcarek J.M.;  
"Cloning and expression of cDNA for a human low-Km, rolipram-sensitive  
cyclic AMP phosphodiesterase.";  
RL Mol. Cell. Biol. 10:2678-2686(1990).  
RN [4]  
RP REVISIONS TO REF. 3.  
RA McLaughlin M.M.;  
RL Submitted (JAN-1991) to the EMBL/GenBank/DDBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (PDE4A7/A6 AND PDE4A8/2EL).  
RX MEDLINE=9529008; PubMed=772058;  
RA Horton T.M., Sullivan M., Houslay M.D.;  
RT "Molecular cloning of a novel splice variant of human type IVA  
(PDE-IVA) cyclic AMP phosphodiesterase and localization of the gene  
to the p13.2-q12 region of human chromosome 19.";  
RL Biochem. J. 308:683-691(1995).  
RN [6]  
RP SEQUENCE FROM N.A. (PDE4A7/A6).  
RX MEDLINE=95194817; PubMed=7888306;  
RA Sullivan M., Burton M., Shakur Y., Marquardsen A., Houslay M.D.;  
RT "Molecular cloning and expression, in both COS-1 cells and S.  
cerevisiae, of a human cytosolic type-IVA, cyclic AMP specific  
phosphodiesterase (PDE-IVA-h6.1).";  
RT Cell. Signal. 6:793-812(1994).  
-1- CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =  
-1- ADENOSINE 5'-PHOSPHATE.  
-1- ENZYME REGULATION: INHIBITED BY ROLIPRAM.  
-1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.  
-1- SUBCELLULAR LOCATION: THE PDE4A1 RD1 ISOFORM HAS PROPENSITY FOR  
CC ASSOCIATION WITH MEMBRANES.  
-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED BY  
CC ALTERNATIVE SPlicing. PDE46 (SHOWN HERE) REPRESENTS A LONG ISOFORM  
CC AND PDE4A1RD1 A SHORT ISOFORM. ISOFORM 2EL PROBABLY REPRESENTS A  
CC NON-FUNCTIONAL SPlice VARIANT. THE PRESENCE OF DIFFERENT N-  
CC TERMINAL REGIONS HAS BEEN LINKED WITH DISTINCT FUNCTIONAL ROLES.  
-1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE  
CC FAMILY.  
-----  

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QY	191	EPKLASFLTPIDIMGLAAAHVDHPGVNOPLIKTNHHLNQNMVLEHNHRST	250
Db	272	TPALEAVTDTLEVLAACATHDVDPGVSQNFQILNTNEALMUNDSVHNHLAVG	331
OY	251	IGMLRESR--LIAHLPKEMTQDIEQQQLGSLLATDINRNEFLTRKALHNKD-----	302
Db	332	FKLQGENCDIFONLSTKQKLSLRMVIDMLATDMSKHMSSLLADLTMVWEKKVTLGV	391
QY	303	LRLEDADDRHFMQIAKCADTCNPCTRIWEMSKWOSERVICEPYROGELEOKFELEISP	362
Db	392	LLLDNYSDRRIQVLOSLVHCAIDLNSPAKPLPLYROWTERIMMAFFQGDRERESGLDISM	451
QY	363	CHQKQDSDIPSQIGFMSYVFLFREWAHFIGNSTLSEMLGHLAHNKAQWKSLLPRQRH	422
Db	452	CDKHTASVEKSQYQGDYHDTAHLWETDAHLWHPD--AQELDUDTLEDNRWNEQSRVP---	505
OY	423	SRGGSGSPDH--DHAGQGTSEEQGD	448

RESULT 15  
YST, CAEEL

AC Q20000;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DF 15-JUL-1998 (Rel. 36, last sequence update)  
 DT 15-JUL-1998 (Rel. 36, last annotation update)  
 DE Probable 3',5'-cyclic phosphodiesterase R153.1 (EC 3.1.4.17)

OC  
Eularloida; *Mezalozia*; Nematoidea; Chromadorea; Rhabditida; Rhabditoidae; *Ploderinae*; Caenorhabditis. NBL1-TaxID=6319

RA  
RL  
Kirsten J.;  
Submitted (JUN-1994)

ND  
SUBLIMED (1955) TO THE BODDENDYK AND GALTIERE: NUCLEOSIDE  
-1 - CATALYTIC ACTIVITY: Nucleoside 3', 5'-CYCLIC PHOSPHATE + H<sub>2</sub>O →  
CC  
CC  
-1 - SIMILARITY: BENOZIDE 5'-PHOSPHATE.  
CC  
FAMILY: STRONG, TO MAMMALIAN TYPE 4 CAMP PHOSPHODIESTERASES.

DR EMBL; U28729; AAA68292.1; -. DR WormPep; R153.1; CB02038. DR InterPro; IPR03607; HIC. DR InterPro; IPR020203; PDBase. DR Pfam; PF0233; PDBase; 1. DR PRINTS; PRO0387; PDIESTERASE1. DR SMART; SM0041; HIC; 1. DR PROSITE; PS00126; PDEASE\_I; 1. KW HYPOTHETICAL PROTEIN; HYDROLASE; cAMP. SEQUENCE 549 AA; 62904 MW; D2EE6F03925DE87 CRC64;

Query Match 21.5%; Score 517; DB 1; Length 549;  
 Best Local Similarity 32.6%; Fred. No. 2.2e-34;  
 Matches 114; Conservative 72; Mismatches 140; Indels 24; Gaps 6

**THIS PAGE BLANK (USPTO)**



RESULT 2  
US-07-688-352C-20  
Sequence 20, Application US/07688352C  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Boud, Michel F.  
REGISTRATION NUMBER: 25-447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: AMINO ACID  
SEQUENCE: GRANDEDNESS: single  
TOPOLOGY: linear  
US-07-688-352C-20

RESULT 3  
US-08-174-379C-20  
Sequence 20, Application US/08474379C  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
TITLE OF INVENTION: PROCESSES  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
STREET: 233 South Wacker Drive/6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,379C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,188  
FILING DATE: 01-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,352C  
FILING DATE: 19-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-379C-20

RESULT 4  
US-07-688-352C-20  
Sequence 20, Application US/07688352C  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Boud, Michel F.  
REGISTRATION NUMBER: 25-447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: AMINO ACID  
SEQUENCE: GRANDEDNESS: single  
TOPOLOGY: linear  
US-07-688-352C-20

RESULT 5  
US-07-688-352C-20  
Sequence 20, Application US/07688352C  
GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,188  
FILING DATE: 01-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,352C  
FILING DATE: 19-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-379C-20

Query Match 58.9%; Score 1419.5; DB 2; Length 498;  
 Best Local Similarity 61.7%; Pred. No. 1.3e-140;  
 Matches 261; Conservative 70; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERGEGILENPPONAKVCMGLDIRGQTYGRAERGSYPPIDFRUNSTYSGIGTK 66  
 DB 62 ORRGATSYDSSBOTALYIRMGLDVRVRSRAGESERGSHPYIDFRIFHSOEIEVSVA 121

QY 67 KVKVLISFORPHASRLRGITQAPHLHEDYLGQARHMLSKVQWMDIFLFDRLT 126  
 DB 122 RNIRRLISFORLSSRFGRGAVSNLNLDDYNGQAKMLEKYGWNWFNDFIFLFDRLT 181

DB 122 RNIRRLISFORLSSRFGRGAVSNLNLDDYNGQAKMLEKYGWNWFNDFIFLFDRLT 181

QY 127 NENSLVLTICHFTNTHGLIHHKLDMLTHRLVMQEDYHSQNPYHNAHADYQAMH 186  
 DB 182 NGNSLVLSTFHFSLHGLIEYHFLDMKLRFLVMOEDYHSQNPYHNAHADYQAMH 241

QY 187 CYLKEPKLASFTPLDMLGILAAAHDDHGVNQPLIKHNLTYKNTSVLENH 246  
 DB 242 CYLKEPKLASFTPLDMLGILAAAHDDHGVNQPLIKHNLTYKNTSVLENH 301

QY 247 WRSTIGMARESLLAHLPKEMTQDIEQOLGSILATDINRNEFLTRKAHNNDKIRLE 306  
 DB 362 DTRRHLVLQMLAKCADICNPCTWELSKWONSEKVEFFHQGDEKKYHGLVSPLCDR 421

QY 367 KOSIPSIQIGMSYIVPFLRWAHFGNSTSENMGHLANKAOKWSLPRQHRSRS 426  
 DB 422 TESIANIQIGEMYLVPLFTWARS-NTRLSQTMGLGHGLINKASWKGLOREQSSEDT 480

QY 427 SGS 429

DB 481 DAA 483

RESULT 4

US-09-146-249A-20

Sequence 20, Application US/09146249A

Patent No. 606240

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF INVENTION: Processes

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146, 249A

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715

FILING DATE: 20-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312-474-0448

RESULT 5

US-08-206-188B-20

Sequence 20, Application US/08206188B

Patent No. 6100025

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF INVENTION: Processes

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/206, 188B

FILING DATE: 01-MAR-1994

CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/5  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 35107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-2474-6300  
TELEFAX: 312-2474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLCULE TYPE: protein  
US-08-206-188B-20

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; NUMBER_OF_SQ_ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ_ID_NO 3
; LENGTH: 320
; TYPE: PRT
; ORGANISM: HOMO sapiens
US-09-330970-3

Query Match 53.2%; Score 1280; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3 1e-126;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28 GDIRURQGQVRAFRRGSPFIDFLRLNSTVSGEGLGKVKRLSFQYFHASRLRG 87
Db 80 GDIRURQGQVRAFRRGSPFIDFLRLNSTVSGEGLGKVKRLSFQYFHASRLRG 139
OY 88 IIPQAPLHLIDEDYLGQARMHSKVGMDFFLFDRLNTNSVNLCHLPNTGLIH 147
Db 140 IIPQAPLHLIDEDYLGQARMHSKVGMDFFLFDRLNTNSVNLCHLPNTGLIH 199

```

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 63:

## SEQUENCE CHARACTERISTICS:

LENGTH: 673 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-474-379C-63

## Query Match

25.1%; Score 604.5; DB 2; Length 673;

Best Local Similarity 33.3%; Pred. No. 9.9e-55; Matches 135; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKKKRMSQISGVKKLHMSSSLTNSIPRGVYKQEDVLAKE--LEDYNNKWLHVFR 274

Db 218 KKKKKRMSQISGVKKLHMSSSLTNSIPRGVYKQEDVLAKE--LEDYNNKWLHVFR 274

QY 122 FRLTNGNSLVYLICH-LFNTIGLILHFKLDMVTLRFLLVMQEDYHSQNPYHNAHAAD 180

Db 275 IAEI-SGNRPLVIMHIFTQERDLKTFKIPVDTLTYLMTLEDHYHADYAHNNHAAD 333

QY 181 VTOAMHQLKEKLAISLPTDILMGLAAMAAAHDVHPGVWQPLIKTNHHLNLQMS 240

Db 334 VVQSTHVLISTPALEAVFTDLEIAAFAASATHDVHPGVSNQFLINTSELALMNDSS 393

QY 241 VLENHHHRSTIGMILRESR--LIAHLPKEMTDIEQQIGSLILATDINRNEFLTRKAHL 298

Db 394 VLENHHHLAVGFLKLUQEEENDITQNLTKKQROSILRKWMDIVLATDKHNMULADIKTMV 453

QY 299 HNKD-----LRLEDAQRHFMQLQIAKCADCNPCRIWEMSKOSERVICEEYROGELE 352

Db 454 EKKVVTSSGVLLDNDYNSDRIQVQLQNMVHCADISNPYKPLQYRQWDRIMEFFRQDRE 513

QY 353 QKFELEISPLCNCQKQDSTSPTIOTGFMSTYIVEFLFREWAHTFGNSTLSENMGHLHAINKAQ 412

Db 514 RERGMEISPMCDKHNASVEKSVQFGFIDIVHPLWEWADLYHD--AQDILDTLEDNREW 571

QY 413 WSLLPQHQHRSQGSSGGPDDHHAQGCTSE-----EGBDS 449

Db 572 YQSTIPO-----SPSPAPDDPEEGROGOTERFOFELTLEEDGES 610

RESULT 8

US-09-146-249A-63

; Sequence 63, Application US/09146249A

; Patent No. 6059240

GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.  
TITLE OF INVENTION: Cloning by Complementation and Related  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146, 249A  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511, 715

## FILING DATE: 20-APR-1990

## ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 25-3856

INFORMATION FOR SEQ ID NO: 63:

## SEQUENCE CHARACTERISTICS:

LENGTH: 673 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-146-249A-63

Query Match

25.1%; Score 604.5; DB 3; Length 673;

Best Local Similarity 33.3%; Pred. No. 9.9e-55; Matches 135; Mismatches 151; Indels 33; Gaps 9;

QY 66 KKKKKRMSQISGVKKLHMSSSLTNSIPRGVYKQEDVLAKE--LEDYNNKWLHVFR 274

Db 218 KKKKKRMSQISGVKKLHMSSSLTNSIPRGVYKQEDVLAKE--LEDYNNKWLHVFR 274

QY 122 FRLTNGNSLVYLICH-LFNTIGLILHFKLDMVTLRFLLVMQEDYHSQNPYHNAHAAD 180

Db 275 IAEI-SGNRPLVIMHIFTQERDLKTFKIPVDTLTYLMTLEDHYHADYAHNNHAAD 333

QY 181 VTOAMHQLKEKLAISLPTDILMGLAAMAAAHDVHPGVWQPLIKTNHHLNLQMS 240

Db 334 VVQSTHVLISTPALEAVFTDLEIAAFAASATHDVHPGVSNQFLINTSELALMNDSS 393

QY 241 VLENHHHRSTIGMILRESR--LIAHLPKEMTDIEQQIGSLILATDINRNEFLTRKAHL 298

Db 394 VLENHHHLAVGFLKLUQEEENDITQNLTKKQROSILRKWMDIVLATDKHNMULADIKTMV 453

QY 299 HNKD-----LRLEDAQRHFMQLQIAKCADCNPCRIWEMSKOSERVICEEYROGELE 352

Db 454 EKKVVTSSGVLLDNDYNSDRIQVQLQNMVHCADISNPYKPLQYRQWDRIMEFFRQDRE 513

QY 353 QKFELEISPLCNCQKQDSTSPTIOTGFMSTYIVEFLFREWAHTFGNSTLSENMGHLHAINKAQ 412

Db 514 RERGMEISPMCDKHNASVEKSVQFGFIDIVHPLWEWADLYHD--AQDILDTLEDNREW 571

QY 413 WSLLPQHQHRSQGSSGGPDDHHAQGCTSE-----EGBDS 449

Db 572 YQSTIPO-----SPSPAPDDPEEGROGOTERFOFELTLEEDGES 610

RESULT 9

US-08-006-188B-63

; Sequence 63, Application US/08206188B

; Patent No. 6100025

GENERAL INFORMATION:  
APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146, 249ACLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511, 715



## CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &amp; No. 6291199ris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Worperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/079, 630

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/577, 492

FILING DATE: 22-DEC-1995

APPLICATION NUMBER: GB 9426227.6

FILING DATE: 23-DEC-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: GB 9512996.1

FILING DATE: 26-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Cherry, David A.

REGISTRATION NUMBER: 35, 099

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 673 amino acids

TYPE: amino acid

TOPOLOGY: unknown

US-09-079-630-35

## Sequence 4, Application US/07688352C

PATENT NO. 5527896

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related

NUMBER OF SEQUENCES: 57

TITLE OF INVENTION: Processes

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp;

STREET: Two First National Plaza, 20 South Clark

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/688, 352C

FILING DATE: 19910419

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/511, 715

FILING DATE: 20-APR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 2547

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 27805/30197

TELEPHONE: (312) 366-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 562 amino acids

TYPE: AMINO ACID

TOPOLOGY: Linear

MOLECULE TYPE: protein

US-07-688-352C-4

## Query Match 24.9%; Score 59.5; DB 4; Length 673;

Best Local Similarity 33.6%; Pred. No. 3.3e-54;

Matches 136; Conservative 84; Mismatches 152; Indels 33; Gaps 10;

Db

Qy 66 KKKVKRLLS---FQRYHASRLLRGITPQAPHLIDDEDYLGQARHMLSKVGMWDFDIFL 121

Db 218 KERKKRPMQSQVKLMLHSSSLNTTSIPRGVTEQEDVLAKE--LEDVNRKGHLVFR 274

Qy 122 FDRLTGNSLVTLILCHFNTGHLHFKLDMTLPRLRPLVYQDYSQHNPYNAHAD 180

Db 275 IABEL-SGNRPLTVIMHTFOERDILKTFKIPVDTLITYLMTLEDHYHADVAHNTHAD 333

Qy 181 VTOAMHCYKLEPKLASFILPDLIMGLLAAAHADVHDHPGVNQPLFLIKTNHHLANLYNMS 240

Db 334 VVOSTHVLSTPRALEAVTDLETLAATFASAHDVHDHPGVNQFLINNSERALMYNDS 393

Qy 241 VLNHHWHRSTIGMRESR--LALHLPKMNTQDIEQQLGSLIATDINRQEFLTRLKAHL 298

Db 394 VLENHHHLAVGFKLQIQQEENDCIFONLTQKROSLRKMVIDIVATDMSKHMLLADLTMV 453

Qy 299 HNKD----LRLDAQDRHFMQIAKCADICNPICRJWEMSKOWSERVCFYROGELE 352

Db 454 ETKVVTSSGVLLDNYNSDRIQVQIYHNCADLSNPTKPLQYRWTDRIMEFQDFDRE 513

Qy 353 QKPELESPLCNQDKSDPSIPIQIGFMSVTEPFLPREWAHTGNTSLPENLGHLAHKQA 412

Db 514 ERGMEISPMCOKHNAVEKSPQVGFIDYVHPLWETWADLVRPD--AQDILDTLEDREW 571

Qy 413 WKSILPROHRSGSSGSPDHDHG--QCTESTE-----EOGDS 449

Db 572 YOSTIPO----SPSPAPDPEEGROQGTGFQFELTLEEDGES 610

Qy 354 KEELEISLCNQDKSDPSIPIQIGFMSVTEPFLPREWAHTGNTSLPENLGHLAHKQA 413

Db 421 ERGMEISPMCOKHNAVEKSPQVGFIDYVHPLWETWADLVRPD--AQDILDTLEDRNWY 478

RESULT 12

US-07-688-352C-4

QY 414 KSLLPR-----QHRSRGSSGSPDHHDH---AGQGTSESEOECDSP 450  
 US 08 942-521B-8  
 Sequence 8, Application US/08942521B  
 Patent No. 5332477  
 GENERAL INFORMATION:  
 APPLICANT: Livli, George P.  
 APPLICANT: McLaughlin, Megan M.  
 APPLICANT: Toppy, Theodore J.  
 TITLE OF INVENTION: Human Brain Phosphodiesterase  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Smithkline Beecham Corporation  
 STREET: Corporate Patents/ P.O. Box 1539  
 CITY: King of Prussia  
 STATE: PA  
 ZIP: 19406-939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-in Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/942-521B  
 FILING DATE: October 2, 1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08446, 386  
 FILING DATE: 22 May 1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08029, 334  
 FILING DATE: 10 March 1993  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth J. Hecht  
 REGISTRATION NUMBER: 41, 824  
 REFERENCE/DOCKET NUMBER: PS0145C1FWC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 277-5009  
 TELEFAX: (215) 270-5050  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 562 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-942-521B-8

Query Match 24.1%; Score 580.5; DB 2; Length 562;  
 Best Local Similarity 31.9%; Pred. No. 2.5e-52; Mismatches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7; Matches 130; Gaps 7;

QY 66 KKKVRLS---FORYPHASRLRGLITFQAPLHLDEQGARHMLSKVGMDFDIFL 121  
 DB 124 KKKKQQLMTOISGVKLMHSSLNNTSISRFGVNTENDHLAKELDNLK--WGLNTFN 180  
 QY 122 FDRLLNGNSLVTLLCHLFWPHGLIHEKIDMVLHREVMQDYHCONPYHNAADV 181  
 DB 181 VAGYSHNRPCTCIMAIFORDLINKTSISDTEVTYMTLHDYHHDVAYINSLRAADV 240  
 QY 182 TOAMHCYKLKPPLASFLTPDIDMIGLILAAAHDYHFGVNOPLIKTNHHLANLYKNSV 241  
 DB 241 AOSTHVLSTLSPALDVFTEELAIAFARAHYDHPAVSNQFLINTNSEALMYNDES 300  
 QY 242 LENHWRSTIGMRESR--LHLHLKEMTQDIEQOLGSLILANDINRONEFLTRKAHLH 299

RESULT 13  
 US 08 942-521B-8  
 Sequence 8, Application US/08942521B  
 Patent No. 5332477  
 GENERAL INFORMATION:  
 APPLICANT: Livli, George P.  
 APPLICANT: McLaughlin, Megan M.  
 APPLICANT: Toppy, Theodore J.  
 TITLE OF INVENTION: Human Brain Phosphodiesterase  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Smithkline Beecham Corporation  
 STREET: Corporate Patents/ P.O. Box 1539  
 CITY: King of Prussia  
 STATE: PA  
 ZIP: 19406-939  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-in Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/942-521B  
 FILING DATE: October 2, 1997  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08446, 386  
 FILING DATE: 22 May 1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08029, 334  
 FILING DATE: 10 March 1993  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Elizabeth J. Hecht  
 REGISTRATION NUMBER: 41, 824  
 REFERENCE/DOCKET NUMBER: PS0145C1FWC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 277-5009  
 TELEFAX: (215) 270-5050  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 562 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-942-521B-8

RESULT 14  
 US-08-474-379C-4  
 Sequence 4, Application US/08474379C  
 Patent No. 5977305  
 GENERAL INFORMATION:  
 APPLICANT: Wiegler, Michael H.  
 APPLICANT: Collelli, John J.  
 TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED PROCESSES  
 NUMBER OF SEQUENCES: 88  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 233 South Wacker Drive/6300 Sears Tower  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-in Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/474, 379C  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/511, 715  
 FILING DATE: 20-APR-1990  
 PRIOR APPLICATION DATA: US 08/206, 188  
 FILING DATE: 01-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/688, 352  
 FILING DATE: 19-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clough, David W.  
 REGISTRATION NUMBER: 36,107  
 REFERENCE/DOCKET NUMBER: 27866/32771  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 474-6300  
 TELEFAX: (312) 474-0448  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 562 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-474-379C-4

Query Match 24.1%; Score 580.5; DB 2; Length 562;  
 Best Local Similarity 31.9%; Pred. No. 2.5e-52; Mismatches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7; Matches 130; Gaps 7;

QY 66 KKKVRLS---FORYPHASRLRGLITFQAPLHLDEQGARHMLSKVGMDFDIFL 121

Db 124 KKKKQQLMTQISGVKKMHSSSLNTSISRCVNTENEDHLAKELDNLK--WGLNIFN 180  
 Qy 122 FDRLTNGNSLVTLILCHLFNTHGLIHFKLDMVTLHRLVMQEDYHSQNPYHNAADV 181  
 Db 181 VAGYSHNRPLCTIMAYAIFOERDLIKTFKISSTDFVYMMTLEDHYHSDAVHNLSLHADY 240  
 Qy 182 TOAMHCYCLKEPLASFLTPDLMGLAANADWDHGVMQNPFLIKTNHHLANLYNMSV 241  
 Do 241 AOSTHVLSTPALDAVFTDLELAIAFAAIIHDVHGVSNQFLINTNSELALMNDSY 300  
 Qy 242 LENHHWSTIGMRESR--LLAHLPKEMTQDIEQQQLGSLLATDINRNEFLTRIKAHLH 299  
 Do 301 LENHHWAVGFKLQQUEECDIFQNLTKQRQTRKVMIDWMLVATDMSKHMSSLADLKTME 360  
 Qy 300 NRD----LRLEDAODRHFMIQIAKCADICNPCTWEMSKWSERVICECFYRQCELEQ 353  
 Do 361 TKKVTSQVLLDNYTDRIQVLRNMHCADLSNPKSLEYRQWTDRLMEEFFQODKER 420  
 Qy 354 KEELEISPLCNOQKDSPSIQIGFMSYIYEPFREWAHFGNSTLSENMLGHHLANKAQ 413  
 Do 421 ERGMETSPMCDDKHTASVEKSVQGVFDYIVHPLWETADLWOPD--AQDILDTLEDNRWY 478  
 Qy 414 KSLLPR----QHRSRGSSGGPDHDH---AGQTESEEGDSP 450  
 Do 479 OSMIPOSPPPLDERSRCQGIMEKFELTLEEESEGPEKEGEGP 525

RESULT 15  
 US-09-146-249A-4  
 ; Sequence data for application US/09146249A

Patent No. 6069240

GENERAL INFORMATION:

APPLICANT: Wigler, Michael H.

APPLICANT: Colicelli, John J.

TITLE OF INVENTION: Cloning by Complementation and Related  
 NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 South Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: United States of America  
 ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/146,249A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/511,715

FILING DATE: 20 APR 1990

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid  
 LENGTH: 562 amino acids

TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-09-146-249A-4

Best Local Similarity 31.9%; Pred. No. 2.5e-52;  
 Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7;

Qy 66 KKKVRLS---FQRYHASRLRGITPQAPLHLDEDYLQGARHMSKVGMMWDFDFL 121  
 Db 124 KKKQQLMTQISGVKKMHSSSLNTSISRCVNTENEDHLAKELDNLK--WGLNIFN 180  
 Qy 122 FDRLTNGNSLVTLILCHLFNTHGLIHFKLDMVTLHRLVMQEDYHSQNPYHNAADV 181  
 Db 181 VAGYSHNRPLCTIMAYAIFOERDLIKTFKISSTDFVYMMTLEDHYHSDAVHNLSLHADY 240  
 Qy 182 TOAMHCYCLKEPLASFLTPDLMGLAANADWDHGVMQNPFLIKTNHHLANLYNMSV 241  
 Do 241 AOSTHVLSTPALDAVFTDLELAIAFAAIIHDVHGVSNQFLINTNSELALMNDSY 300  
 Db 301 LENHHWAVGFKLQQUEECDIFQNLTKQRQTRKVMIDWMLVATDMSKHMSSLADLKTME 360  
 Qy 242 LENHHWSTIGMRESR--LLAHLPKEMTQDIEQQQLGSLLATDINRNEFLTRIKAHLH 299  
 Do 361 TKKVTSQVLLDNYTDRIQVLRNMHCADLSNPKSLEYRQWTDRLMEEFFQODKER 420  
 Qy 354 KEELEISPLCNOQKDSPSIQIGFMSYIYEPFREWAHFGNSTLSENMLGHHLANKAQ 413  
 Do 421 ERGMETSPMCDDKHTASVEKSVQGVFDYIVHPLWETADLWOPD--AQDILDTLEDNRWY 478  
 Qy 414 KSLLPR----QHRSRGSSGGPDHDH---AGQTESEEGDSP 450  
 Do 479 OSMIPOSPPPLDERSRCQGIMEKFELTLEEESEGPEKEGEGP 525

Search completed: September 13, 2002, 12:05:51  
 Job time: 252 sec

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OM protein - protein search, using sw model

Run on: September 13, 2002, 11:59:44 ; Search time 31.9 Seconds (without alignments)  
1566.872 Million cell updates/sec

Title: US-09-471-459A-5  
Perfect score: 2408  
Sequence: 1 MSCLMYVERCGTLETFENDQN.....PDHDHAGQGTSEEEQEGDSP 450

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searches: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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13: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

15: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*

16: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

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20: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2408	100	0	Amino acid sequence
2	2408	100	0	Human type 7B phosphodiester
3	2408	100	0	Human phosphodiester
4	2234	92	8	Long phospho
5	219.5	92	2	Amino acid sequence
6	219.2	91	0	Amino acid sequence
7	2166	90	0	Amino acid sequence
8	2165.5	89	9	Amino acid sequence
9	2121	88	1	Amino acid sequence
10	1990.5	82	7	Amino acid sequence
11	1865	77	5	Human phosphodiester

## ALIGNMENTS

GenCore version 4.5  
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2002, 11:59:44 ; Search time 31.9 Seconds  
 (without alignments)  
 1566.872 Million cell updates/sec

Title: US-09-471-459A-5  
 Perfect score: 2408  
 Sequence: I MSCLAVVERGEETILFENPDQN. .... PDHDHAGQGTESEEGDSP 450

Scoring table: BL2SUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database : A\_Geneseq\_032802:  
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 2: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1981.DAT: \*  
 3: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1982.DAT: \*  
 4: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1983.DAT: \*  
 5: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1984.DAT: \*  
 6: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1985.DAT: \*  
 7: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1986.DAT: \*  
 8: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1987.DAT: \*  
 9: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1988.DAT: \*  
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 11: /\$SDSL/gcdata/hold-geneseq/geneseqp-emb1/AA1990.DAT: \*  
 12: 1430 59.4 268 21 AAY93593 Amino acid sequence  
 13: 1430 59.4 288 21 AAY93569 Amino acid sequence  
 14: 1419.5 58.9 498 20 AAY49808 Amino acid sequence  
 15: 1419.5 58.9 498 20 AAY49808 Amino acid sequence  
 16: 1419.5 58.9 498 21 ARB20619 Human phosphodiesterase  
 17: 1280 53.2 432 22 ARB16367 Human novel secreted  
 18: 1280 53.2 320 22 ARB36504 Human short phospho  
 19: 771 32.0 211 22 ARU23004 Novel human enzyme  
 20: 771 32.0 211 22 ARU18881 Rat and cardiac  
 21: 771 32.0 211 22 ARU17039 Human novel secreted  
 22: 604.5 25.1 507 21 AAY9395 Amino acid sequence  
 23: 604.5 25.1 518 22 ARB61185 Human PDE4B protease  
 24: 604.5 25.1 673 20 ARY49827 Human dunc-1-like P  
 25: 604.5 25.1 673 21 ARB20038 PPDE3 human dunc-1  
 26: 604.5 25.1 673 21 AAY93997 Amino acid sequence  
 27: 604.5 25.1 673 22 ARM51411 Human phosphodiesterase  
 28: 604.5 25.1 704 22 ARB06364 Novel human diagno  
 29: 604.5 25.1 745 21 AAY93996 Amino acid sequence  
 30: 604.5 25.1 929 22 ARG65580 Amino acid sequence  
 31: 604.5 25.1 930 21 AAY84876 Amino acid sequence  
 32: 604.5 25.1 1002 21 AAY84878 Amino acid sequence  
 33: 604.5 25.1 1066 21 ARY84877 Amino acid sequence  
 34: 603.5 25.1 517 22 ARB61186 Human phosphodiesterase  
 35: 603.5 24.9 674 17 ARY99743 Human phosphodiesterase  
 36: 598.5 24.9 1029 22 ARG655779 Amino acid sequence  
 37: 580.5 24.1 562 12 ARR14836 "Dunce"-like phospho  
 38: 580.5 24.1 562 17 ARW00090 Rat dunce-like protein  
 39: 580.5 24.1 562 20 ARY49803 Rat dunce-like protein  
 40: 580.5 24.1 562 21 ARB20614 Plasmid pRATDPD 2.  
 41: 580.5 24.1 564 22 ARB06745 Rat cAMP-specific  
 42: 580.5 24.1 659 22 ARB04741 Rat cAMP-specific  
 43: 580.5 24.1 721 22 ARB0446 Rat cAMP-specific  
 44: 580.5 24.1 736 22 ARB04743 Rat cAMP-specific  
 45: 567.5 23.6 564 15 ARB60605 Brain low Km, cAMP

XX	PS Disclosure: Page 45-47; 104pp; English.	XX	KW Human; type 7B phosphodiesterase; PDE7B; enzyme.
XX	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbent assay (ELISA)).	XX	OS Homo sapiens.
XX	Sequence 450 AA;	XX	PN JP200128680-A.
XX	Query Match 100.0%; Score 2408; DB 21; Length 450; Best Local Similarity 100.0%; Pred. No. 2.3e-227; Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	PD 04-SEP-2001.
QY 1 MSCLMVERCGTILFNPDNACKVCMGLGDIRLKGOTGYRAERGRGSYFPIDERLLNSTTYS 60	QY 1 MSCLMVERCGTILFNPDNACKVCMGLGDIRLKGOTGYRAERGRGSYFPIDERLLNSTTYS 60	XX	PF 03-MAR-2000; 2000JP-0058159.
DB 1 msclmvercgeilfnpdpnakcvecmglgdirlkqgtvraergrgsyfpidfrlnsttys 60	DB 1 msclmvercgeilfnpdpnakcvecmglgdirlkqgtvraergrgsyfpidfrlnsttys 60	XX	PR 03-MAR-2000; 2000JP-0058159.
QY 61 GEIGTKKKVKKLRSQFYHASRLRGTPQAPAHLDUDYLGQARIMLSKVGMDWDF 120	QY 61 GEIGTKKKVKKLRSQFYHASRLRGTPQAPAHLDUDYLGQARIMLSKVGMDWDF 120	XX	PA (TANABE ) TANABE SEIYAKU CO.
DB 61 geigtkkkvkklsfqyhasrlrgtpqaphldedqgqarhmlskvgmwfdf 120	DB 61 geigtkkkvkklsfqyhasrlrgtpqaphldedqgqarhmlskvgmwfdf 120	XX	DR WPI: 2001-610057/70.
QY 121 LFDRLTNGNSLVTLICHLNTHGLIHHKLDWFLHRLFLWVQEDYHSQNPYHNAHAAD 180	QY 121 LFDRLTNGNSLVTLICHLNTHGLIHHKLDWFLHRLFLWVQEDYHSQNPYHNAHAAD 180	XX	DR NPSDB; AAT0009.
DB 121 lfdrltngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	DB 121 lfdrltngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	XX	PT New phosphodiesterase for use in the development of inhibitors of high selectivity and drugs of low side effect -
QY 122 Ifaritrngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	QY 122 Ifaritrngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	XX	XX
DB 122 ifaritrngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	DB 122 ifaritrngnsvlitchlnthglhkhldwflhrlflwvqedyhsqnpynhnaad 180	XX	PS Claim 2; Page 12-14; 18pp; Japanese.
QY 181 VTOQAMHCKYIKEPKLASFLTPDLMGLLAAAHVDHFGVNOPLFLIKINHHLNLYQMS 240	QY 181 VTOQAMHCKYIKEPKLASFLTPDLMGLLAAAHVDHFGVNOPLFLIKINHHLNLYQMS 240	XX	CC The present sequence is the protein sequence for human type 7B phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the development of inhibitors of high selectivity and drugs of low side effects.
DB 181 vtqamhckyikeplasfltpdlimgliaaaahvdhfgvnpflkthlnlyqms 240	DB 181 vtqamhckyikeplasfltpdlimgliaaaahvdhfgvnpflkthlnlyqms 240	XX	CC
QY 241 VLENHHRHRSIGMRESRLAHLPEKMDQIPEQQLGSLILATDINRNEELTRKHLHN 300	QY 241 VLENHHRHRSIGMRESRLAHLPEKMDQIPEQQLGSLILATDINRNEELTRKHLHN 300	XX	CC
DB 241 vlenhhrhrtsgmresrlahlpkmdqieqqlgsilatdinqnefltrkahn 300	DB 241 vlenhhrhrtsgmresrlahlpkmdqieqqlgsilatdinqnefltrkahn 300	XX	CC
QY 301 KDLRLDAODRHFMIQIAKCADCNPWRWENSKOSRVERVCEFYFROGELEQFLETS 360	QY 301 KDLRLDAODRHFMIQIAKCADCNPWRWENSKOSRVERVCEFYFROGELEQFLETS 360	XX	CC
DB 301 kdrlledaqdrhmlqiackadcnpcnwenskqswservecefyqgeleqfleis 360	DB 301 kdrlledaqdrhmlqiackadcnpcnwenskqswservecefyqgeleqfleis 360	XX	CC
QY 421 HRSRGSSGSGPDHDHAGOSTEREQGSP 450	QY 421 HRSRGSSGSGPDHDHAGOSTEREQGSP 450	XX	CC
DB 421 hrsrgssgspdhhaqgtteseqgsp 450	DB 421 hrsrgssgspdhhaqgtteseqgsp 450	XX	CC
RESULT 2	RESULT 3	XX	CC
ID AAG78915	ID AAT08675	XX	CC
AC AAG78915;	AC AAT08675	XX	CC
XX	XX	XX	CC
DE 19-DEC-2001 ( first entry)	DE Human type 7B phosphodiesterase, PDE7B.	XX	AC AAU08675;
XX	XX	XX	XX

DE	Human phosphodiesterase type 7B #1.
XX	
KW	Human; phosphodiesterase type 7B; cardiovascular disease; asthma; allergy; inflammatory disease; immun-related disorder; cardiovascular; antiasthmatic; antiallergic; immunosuppressive; antiinflammatory.
KW	Homo sapiens.
XX	
XX	W020162940-A2.
PD	30-AUG-2001.
PR	20-FEB-2001; 2001WO-EP01058.
PR	21-FEB-2000; 2000EP-010355.
PA	(MERCK ) MERCK PATENT GMBH.
PI	Kluxen F, Hentsch B;
XX	
DR	WPI; 2001-570636/64.
N-PSDB; AAC13248.	
XX	
PT	Phosphodiesterase 7B proteins and nucleic acids, useful for preventing, diagnosing and treating, e.g. asthma, inflammation and allergies.
XX	
PS	Claim 1; Page 36-37; 40pp; English.
XX	
CC	The invention relates to a novel human Phosphodiesterase type 7B polypeptide and the nucleic acid that encodes it. The protein and nucleic acid may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate phosphodiesterase 7B (P7B) expression. For example, the protein and nucleic acid may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P7B by expressing inactive proteins or to supplement the patients own production of P7B. The nucleic acids may be used to produce P7B polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The nucleic acid and its complements may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The P7B polypeptides may also be used as antigens in the production of antibodies against P7B and in assays to identify modulators of it's expression and activity. The anti-P7B antibodies and antagonists may also be used to down regulate expression and activity. The anti-P7B antibodies may also be used as diagnostic agents for detecting the presence of P7B in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). Disorders that may be prevented, diagnosed and/or treated by the above methods include, for example cardiovascular disease, asthma, allergy, inflammation, and immune-related disorders. The present sequence represents a human phosphodiesterase 7B.
XX	
SQ	Sequence 450 AA:
Query Match	100 %; score 2408; DB 22; Length 450;
Best Local Similarity	100 %; Pred. No. 2; 3e-227; Indels 0; Gaps 0;
Matches	450; Conservative 0; Mismatches 0; Gaps 0;
OY	
1	MSCLMVERCGERGELFENDPDKNAVKCVCMLGDIRLRLRGTVRERRGSPFPIDFLRLNSTKS 60
Db	1 msclmvercgergelfendpdknakcvmlgdirlrlrgtvrerrgspfpidflrlnstys 60
OY	61 GEIGKKKKVRLSLSPQRYFASRLRGITQAPHLDEEYLGQARHMSKRVGMDFDIF 120
Db	61 geigkkkkvrlslspqrifasrlrgitqlqaphldeeylgqarhmskvqmgwfdf 120
OY	121 LFDRLLTNGNSLVTLCHLFNTHGLIHFHKIDMVTLRFELMVOEYHSQNPYHNAHA 180
Db	121 lfdrlltngnslvttlchlfnthyglifhkidmvtlfelmvoyhsqnpvhnaahd 180

CC atopic diseases', autoimmune encephalomyelitis, organ transplantation, salt retention in nephrotic syndrome and erectile dysfunction.  
 XX

Sequence 502 AA;

Query Match Best local Similarity 99.1%; Score 2234; DB 22; Length 502; Matches 419; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 28 GDTLRLGQTVGRERRASVPPFDLFLRNLNSTVMSGEGTKKVRLSFRYFHASRLRG 87  
 Db 80 gdirlrsgqgreraeqsyppfdflinstygsigtgkkykrifryhasrlrg 139

QY 88 IIPQAPHLDEDYLGOARHMLSKVQMWDFDIFLFDLRTNGNSLVTLLCHLFNTHGLTH 147  
 Db 140 iipqaphilidedylgarhmlskvqmwdfafiflalrtngsntvlchlifothglhh 199

QY 148 FKLMVWLRELYWQDHYHSONPYINAVADYQAMCYLKEPLASFLPDLIMGL 207

Db 200 fkldmvwlrelywqdyhsqnpynnavadvyqamcyikeplasflpdlimgl 259

QY 208 LAAAHADHDYDHPYVNOPLKIKHHHLNLXKQNSVLENHFRSTGMLRSERLAAHPLKEM 267  
 Db 260 laaaahdhdpyvnpqflikthngalyqmsvlenhfrstgmlrserrlalnplkem 319

QY 268 TQREQQLGSLTIAIDNQBLFLTRKALHANKDRLERADQDHFMQIALKCADICNP 327

Db 320 tqdieqqlgslatldinqnqeflrlkahnkdlrldaqdhfmqiaawcdicnp 379

QY 328 CRIWEMSKQWSERVICEEYFROGELEOKFEELEISPLCNOQDSPSIQTGFMSSIVEPLFR 387  
 Db 380 criwemskqwservceefyrgleqkfleisplcnqkqkdsipqfqmsyiveplfr 439

QY 388 EWAHTGNTSENMLGHAINKAQWSLPRQHRSRGSSGSDDHQAQGESEEDG 447  
 Db 440 ewahftgntisenmlghainkaqwsllprqhsrgssgspdhagqgteseedg 499

QY 448 DSP 450

Db 500 dsp 502

RESULT 5

ID AAY93575 standard; Protein: 451 AA.

XX AAY93575;

XX DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

KW OS Synthetic.

XX

Key-difference Location/Qualifiers

FT 12 /label= Val, Ile

FT 16 /label= Ser, Asn

FT 18 /label= Glu, Asp

FT 20 /label= Ser, Val, Asn, Ala

FT 21 /label= Ser, Val, Asn, Ala

FT 30 /label= Val, Ile

FT 39 /label= Pro, Arg

FT 56 /label= Pro, Arg

FT misc-difference /label= Asn, Ser

FT misc-difference /label= GLY, His, Ser, Gln

FT misc-difference /label= His, Tyr

FT misc-difference /label= Thr, Met

FT misc-difference /label= Ser, Thr

FT misc-difference 168 /label= GLY, His, Ser, Gln

FT misc-difference 169 /label= GLY, His, Ser, Gln

FT misc-difference 307 /label= GLY, His, Ser, Gln

FT misc-difference 350 /label= Glu, Asp

FT misc-difference 379 /label= Asp, Ala, Asn, Val

FT misc-difference 391 /label= Ser, Thr

FT misc-difference 404 /label= His, Arg

FT misc-difference 418 /label= GLY, Ser

FT misc-difference 435 /label= Pro, Arg, Ser, Asn

FT misc-difference 419 /label= Ser, Thr

FT misc-difference 423 /label= His, Arg

FT misc-difference 435 /label= Ser, Arg

FT misc-difference 438-440 /label= His, Leu

FT misc-difference /note= "these residues are either Gln-Gly-Pro or Pro-Ala-Pro"

FT misc-difference 442-443 /note= "these residues are either Ser-Glu or Thr-Leu"

FT misc-difference 446 /note= "optionally absent"

FT misc-difference 449-450 /note= "these residues are either Asp-Ser or Ala-Thr"

FT PN EP1018559-A1.

XX 12-JUL-2000.

XX PD 09-NOV-1999; 99EP-0308902.

XX PR 23-DEC-1998; 98GB-008603.

XX PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ ) PIZZER LTD.

PA (PFIZ ) PIZZER INC.

XX PI Fidock M;

XX DR WPI; 2000-433274/38.

XX PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing, diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity.

XX Disclosure; Page 75-78; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV.









Query Match	88.1%	Score 2121; DB 21; Length 437;	XX
Best Local Similarity	91.9%	Pred. No. 3_1e-199; 1; Mismatches 23; Indels 12; Gaps 6;	CC
Matches	411; Conservative	1; Mismatches 23; Indels 12; Gaps 6;	CC
Db	1 msclmvercgekxlfexpq-xcvcvmlgdxrlrqgqyaerrgyspfidrlinttxs	59	CC
Qy	61 GEITKKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 120	60	CC
Db	60 geitkkkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 119	60	CC
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	121	CC
Db	120 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 178	120	CC
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	181	CC
Db	179 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 238	179	CC
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	241	CC
Db	239 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 298	239	CC
RESULT	10		XX
Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360	Qy	Query Match 82.7%; Score 1990.5; DB 21; Length 413;
Db	299 kdlrle-xqdrfmqlqalkcadicnccriverskyservceefyrgxleqkfleis 357	Db	Best Local Similarity 90.8%; Pred. No. 1.8e-186; 1; Mismatches 5; Indels 35; Gaps 16;
Qy	361 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Qy	Matches 406; Conservative 1; Mismatches 5; Indels 35; Gaps 16;
Db	358 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 416	Db	1 msclmvercge-ife---pkvcvmlgdrxrlrqgqy-aerrgyspfidrlint-s 51
Qy	421 HSRGSSGSGPBDHAGQGTSEEEQEG 447	Qy	61 GEITKKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 120
Db	417 hrxxgsx-----dxa - gxeqeqg 435	Db	60 geitkkkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 110
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Db	288 kdlrle-xqdrfmqlqalkcadicnccriverskyservceefyrg-leqkfleis 344	Db	288 kdlrle-xqdrfmqlqalkcadicnccriverskyservceefyrg-leqkfleis 344
Qy	361 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Qy	361 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420
Db	345 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 399	Db	345 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 399
Qy	421 HSRGSSGSGPBDHAGQGTSEEEQEG 447	Qy	421 HSRGSSGSGPBDHAGQGTSEEEQEG 447
Db	400 hr-rgsda-----geeqeqg 412	Db	400 hr-rgsda-----geeqeqg 412
RESULT	11		XX
Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360	Qy	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
Db	300 kdlrle-xqdrfmqlqalkcadicnccriverskyservceefyrg-leqkfleis 345	Db	The enzyme sequence is derived from a formula of the invention. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
Qy	302 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360	Qy	Sequence 413 AA;
Db	299 kdlrle-xqdrfmqlqalkcadicnccriverskyservceefyrgxleqkfleis 357	Db	Qy 121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180
Qy	362 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	359 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 416	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	422 HSRGSSGSGPBDHAGQGTSEEEQEG 448	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	418 hrxxgsx-----dxa - gxeqeqg 436	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	363 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	354 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 415	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	423 HSRGSSGSGPBDHAGQGTSEEEQEG 449	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	419 hrxxgsx-----dxa - gxeqeqg 437	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	364 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	355 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 416	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	424 HSRGSSGSGPBDHAGQGTSEEEQEG 450	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	420 hr-rgsda-----geeqeqg 438	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	365 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	356 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 417	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	425 HSRGSSGSGPBDHAGQGTSEEEQEG 451	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	421 hr-rgsda-----geeqeqg 439	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	366 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	357 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 418	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	426 HSRGSSGSGPBDHAGQGTSEEEQEG 452	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	422 hr-rgsda-----geeqeqg 440	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	367 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	358 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 419	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	427 HSRGSSGSGPBDHAGQGTSEEEQEG 453	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	423 hr-rgsda-----geeqeqg 441	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	368 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	359 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 420	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	428 HSRGSSGSGPBDHAGQGTSEEEQEG 454	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	424 hr-rgsda-----geeqeqg 442	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	370 PLCNQOKDSIPSTQIOPGMSYIYEPFLFREWAHTGNSTLSENNMLGHANKAOWKSLLPQ 420	Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167
Db	361 plcnqkdsipsiqigfmxnyiyeplfrewaxftgnstlsemlxhahnkawksll-xq 421	Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240
Qy	429 HSRGSSGSGPBDHAGQGTSEEEQEG 455	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	425 hr-rgsda-----geeqeqg 443	Qy	241 VLENHHRSTGMLRERLLAHLPKEMTQDIEQQLGSLLATDINQNEFLTRKALHN 300
Qy	121 LFDRLTNQNSLVTLCLHLFNTFGLIHLHFKLDMVTLHFLVMQEDYHSQNPYHNAHAAD 180	Db	228 vlenhhrstgmlrersllahlpkemtdieqqlgsllatdinqnreflrikahn 287
Db	111 lfdrltngnsivtllchlnfxnglhlhfklnwtlnflvlnqedyh-x-npyhnavhaad 167	Qy	301 KDLRLEDQDRHFMQLQALKCADICNCPRIWMSKOMSERVEEFYRQEGELEQKFELES 360
Qy	181 VTOAMHCKKKVKKRRLSFORFHASRLRQIIPQPLHLDEDYIGQARHMLSKVGMWDFIF 240	Db	168 vtrqamhckkkvkkrlsfqyfhasrlrqipaplhldedylqgarhmlskvqwfif 227
Db	168 vtrqamhckkkv		

kw asthma; allergy; inflammatory disease; immune-related disorder;  
 kw cardiovascular; antiasthmatic; antiallergic; immunosuppressive;  
 kw antiinflammatory.  
 xx Homo sapiens.  
 fh Key Location/Qualifiers  
 ft Misc-difference 188 /note= "Encoded by GAR"  
 ft Misc-difference 188 /label= "Unknown" /note= "Encoded by CMC"  
 ft Misc-difference 387 /label= "Unknown" /note= "Encoded by GNN"  
 xx w0200162940-a2.  
 xx pn 30-aug-2001.  
 xx pf 20-feb-2001; 2001wo-e001858.  
 xx dr 21-feb-2000; 2000ep-0103655.  
 xx pa (merck ) merck patent gmbh.  
 pt Kluxen F, Hentsch B;  
 xx ps claim 1; page 39-40; 40pp; english.  
 cc the invention relates to a novel human phosphodiesterase type 7b polypeptide and the nucleic acid that encodes it. the protein and nucleic acid may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate phosphodiesterase 7b (p7b) expression. for example, the protein and nucleic acid may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of p7b by expressing inactive proteins or to supplement the patient's own production of p7b. the nucleic acids may be used to produce p7b polypeptides, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. the nucleic acid and its complements may also be used as dna probes in diagnostic assays to detect cc therefore which patients may be in need of restorative therapy. the p7b polypeptides may also be used as antigens in the production of cc antibodies against p7b and in assays to identify modulators of it's cc expression and activity. the anti-p7b antibodies and antagonists may also be used to down regulate expression and activity. the anti-p7b cc antibodies may also be used as diagnostic agents for detecting the presence of p7b in samples (e.g. by enzyme linked immunosorbent assay (elisa)). disorders that may be prevented, diagnosed and/or treated by the above methods include, for example cardiovascular disease, asthma, cc allergy, inflammation, and immune-related disorders. the present sequence represents a human phosphodiesterase 7b.  
 xx sq sequence 391 aa;

Query Match 77.5%; Score 1865; DB 22; Length 391;  
 Best Local Similarity 92.7%; Pred. No. 3.4e-174; Mismatches 354; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

Qy 52 RLLNSPTTYSCEIGIKKKVRLLSQTYRTHASRLRLGTTIPQAPLHLIDEDVQARMLSK 111  
 Db 10 rllnstsyygeigkkkvrlsifqryhasrlrlgqipphihldediyqgashmk 69  
 Qy 112 VGMWDFDIFLDRITGNSLVTLCLHFLNTHGLIHHFKLDMVTLHRLFLVWQEDYHSQNP 171

Db 70 vpmwdfdfiflfdrltqnsitvlchlfthgq1hhfkidmvilhrflvmyqedyisnp 129  
 Qy 172 YHNAVHADYQAMHQLKEKLAFLPFDIMGLMAAAHYDHGCVNQPLIKTNHH 231  
 Db 130 yhnavhadvtqamhcyikeplasflptpldimigliaaaahdvhpgvnaqpliflxh 189  
 Qy 232 LANLYQMSVLENHHRSTGMLRSRSLAHLREMTDIEQGLSLTALDINRONEFL 291  
 Db 190 lanlyqmsvlenhhrstgmlrsrslahlremtdieqglsgsialtdinrqnefl 249  
 Qy 292 TRUKAHHNKDLRLEAQDRIFMQLAKCADCINPCRLWEMSKWRRVERCEBFYQGEL 351  
 Db 250 trikahhnkdlrleaqdrifmqlakcadcnpcrlwemskwrrvercebfyqgel 309  
 Qy 352 EQKFELEISPLCNOQKDSKSIQIGFMSIVPEFREWAHFGNTISENNMLGHLAHNKA 411  
 Db 310 egkfgleisplicnqkdskipsiqifgmsivpepalpgmahnftgnstqrtcwtfahnkq 369  
 Qy 412 QWKSLLPRQHRSRGSSGGDH 433  
 Db 370 qwksllpsssteagaalaxgldh 391

result 12  
 id AX93593 standard; protein; 268 AA.  
 xx  
 xx ac AY93593;  
 xx dt 25-sep-2000 (first entry)  
 xx de amino acid sequence of a human phosphodiesterase enzyme.  
 xx kw phosphodiesterase; pde-xiv; enzyme.  
 xx os homo sapiens.  
 xx ep018559-al.  
 xx pd 12-jul-2000.  
 xx pf 09-nov-1999; 99ep-0308902.  
 xx pr 23-dec-1998; 98gb-0028903.  
 xx pr 17-sep-1999; 99gb-0022123.  
 xx pa (pfiz ) pfizer ltd.  
 xx pa (pfiz ) pfizer inc.  
 xx pt fidock m;  
 xx dr wpi: 2000-433274/38.  
 xx pt nucleic acids encoding recombinant phosphodiesterase (pde)-xiv enzymes, pt nucleic acids encoding recombinant phosphodiesterase (pde)-xiv enzymes, pt inappropriate pde-xiv expression and/or activity -  
 xx disclosure; page 87-88; 104pp; english.  
 xx  
 cc the present sequence represents a phosphodiesterase (pde) enzyme. the phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pde-xiv expression. for example, the polynucleotide may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of pde-xiv. they may also be used to study the expression and function of pde-xiv polypeptides and their role in metabolism. the pde-xiv polypeptides may be used as antigens in the production of antibodies against pde-xiv and in assays to identify modulators (agonists and antagonists) of pde-xiv expression and activity. the anti-pde-xiv antibodies and pde-xiv antagonists may also be used to down regulate pde-xiv expression and activity (i.e. the pde-xiv gene and/or expression product may be

CC	used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity.
CC	The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
XX	Sequence 268 AA;
Query Match	59.4%; Score 1430; DB 21; Length 268;
Best Local Similarity	100.0%; Pred. No. 9; 3e-132;
Matches	268; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Db	1 MSCIMVERCGEITLFENPDNAKCVCMGLGDIRLRGQTYRAERGSYPPFIDRLLNSTYS 60
Db	1 msclmvercgeitlfenpdnaqcvcmglgdirlrqgtyraergsyppfdrllnstys 60
Qy	61 GEIGTKKKVKRISFQRYFHASRLRIGCIPQPLHILDEDYLGQARHMLSKVGMADF 120
Db	61 geigtkkkvkrilsfqyfhasrlrlrigcipqaphilidedyqgarhmlskvqmwdf 120
Qy	121 LFDRLTNGNSLVTLLCILFNLNFGHLIHFKLDAVTLHRLFLVMQEDYHSQNYHNAVHAAD 180
Db	121 lfdrltngnslvttllciflnftnglifhfkldmvtlfhflmvqedyhsqnyhyavhaad 180
Qy	181 VHQAMHCVLKEPKLASFLTPUDIMGLHAAAHDVPHQGVNQPLFLKTNNHHLNLYQMS 240
Db	181 vHQAMHCVLKEPKLASFLTPUDIMGLHAAAHDVPHQGVNQPLFLKTNNHHLNLYQMS 240
Qy	241 VLENHHRSTGMLRESRLAHLPKEMT 268
Db	241 vlenhhrstgmlresrlahlpkemt 268
RESULT	13
AAV93568	
ID	AAV93568 standard; Protein; 288 AA.
AC	AAV93568;
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a human phosphodiesterase enzyme.
KW	Phosphodiesterase; PDE-XIV; human; enzyme.
XX	
OS	Homo sapiens.
XX	
EP1018559-A1.	
XX	
PD	12-JUL-2000.
XX	
PF	09-NOV-1999; 99EP-0308902.
XX	
PR	23-DEC-1998; 98GB-0028603.
XX	
PR	17-SEP-1999; 99GB-0022123.
XX	
PA	(PFIZ ) PFIZER LTD.
PA	(PFIZ ) PFIZER INC.
XX	
PT	Ridock M;
XX	
DR	WPI; 2000-433274/38.
XX	
N-PSDB;	AAA46650.
XX	
PR	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing, diagnosing and treating diseases associated with inappropriate PDE-XIV expression and/or activity -
XX	
PS	Disclosure; Page 42-44; 104pp; English.
XX	
CC	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC	phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the Polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV.
CC	CC polypeptides to study the expression and function of PDE-XIV and activity, (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
CC	CC and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and CC may be used as antigens in the production of antibodies against PDE-XIV and activity, (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).
XX	Sequence 288 AA;
Query Match	59.4%; Score 1430; DB 21; Length 288;
Best Local Similarity	100.0%; Pred. No. 1e-131;
Matches	268; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Db	1 MSCIMVERCGEITLFENPDNAKCVCMGLGDIRLRGQTYRAERGSYPPFIDRLLNSTYS 60
Db	1 msclmvercgeitlfenpdnaqcvcmglgdirlrqgtyraergsyppfdrllnstys 60
Qy	61 GEIGTKKKVKRISFQRYFHASRLRIGCIPQPLHILDEDYLGQARHMLSKVGMADF 120
Db	61 geigtkkkvkrilsfqyfhasrlrlrigcipqaphilidedyqgarhmlskvqmwdf 120
Qy	121 LFDRLTNGNSLVTLLCILFNLNFGHLIHFKLDAVTLHRLFLVMQEDYHSQNYHNAVHAAD 180
Db	121 lfdrltngnslvttllciflnftnglifhfkldmvtlfhflmvqedyhsqnyhyavhaad 180
Qy	181 VHQAMHCVLKEPKLASFLTPUDIMGLHAAAHDVPHQGVNQPLFLKTNNHHLNLYQMS 240
Db	181 vHQAMHCVLKEPKLASFLTPUDIMGLHAAAHDVPHQGVNQPLFLKTNNHHLNLYQMS 240
Qy	241 VLENHHRSTGMLRESRLAHLPKEMT 268
Db	241 vlenhhrstgmlresrlahlpkemt 268
RESULT	14
AAW00034	
ID	AAW00094 standard; Protein; 498 AA.
XX	
AC	AAW00094;
XX	
DT	09-OCT-1996 (first entry)
XX	
PR	cAMP phosphodiesterase encoded by plasmid PTM2 (ATCC 68601).
XX	
KW	Human; glioblastoma cell; heat shock sensitivity; Phosphodiesterase;
KW	deficient yeast strain 32D; PTM2; rat DDP phosphodiesterase; pde1-; bovine Ca2+-calmodulin dependent cAMP phosphodiesterase; heart; plasmid; RAS2(val19); pde2-; PTM3; PTM72; PRATDPD; pjc99; rolipram sensitive.
KW	
PT	Ridock M;
XX	
OS	Homo sapiens.
XX	
PN	US5527896-A.
XX	
PD	18-JUN-1996.
XX	
PR	20-APR-1990; 900S-0511715.
XX	
PR	19-APR-1991; 91US-0688352.
PR	20-APR-1990; 900S-0511715.

PA (COLD-) COLD SPRING HARBOR LAB.  
 XX  
 PT Colicelli JJ, Wigler MH;  
 XX  
 DR WPI; 1996-29902/30.  
 DR N-FSDB; AAT34376.  
 XX  
 PT DNA mols. isolated from human glioblastoma cells - encode  
 PT RAS-related or cyclic nucleotide phosphodiesterase proteins  
 XX  
 PS Claim 4; Column 67-70; 101pp; English.  
 XX  
 CC The sequences given in AAW00092-94 are encoded by plasmid fragments  
 CC which contain human glioblastoma cell cDNA inserts which are capable of  
 CC correcting the heat shock sensitivity of the phosphodiesterase  
 CC deficient yeast strain 10DAB. Several cDNAs were isolated and  
 CC sequenced. PTM22 encodes a novel human gene. From computer analysis,  
 CC PTM22 putatively encodes a protein homologous to various cAMP  
 CC phosphodiesterases, such as the bovine Ca<sup>2+</sup>/calmodulin dependent cAMP  
 CC phosphodiesterase and the rat DPB phosphodiesterase. Sequences related  
 CC to PTM22 were found to be expressed in human heart. Plasmid PTM22 was  
 CC unable to correct the heat shock sensitivity of RAS2(V119) yeast  
 CC strains. It thus appears that the pde1- and pde2- yeast strain 10DAB  
 CC is more sensitive to phenotypic reversion by mammalian cAMP  
 CC phosphodiesterase clones than is the RAS2(V119) yeast strain. The  
 CC inserts in the plasmids PTM3 and PTM22 were also characterized. These  
 CC two different cAMP phosphodiesterase cDNAs were found to be closely  
 CC related to, but distinct from, the PRADP insert and the PRC99 insert.  
 CC Biochemical analysis of cell lysates has established that the cDNAs of  
 CC PTM3 and PTM22, pJC44x and PRADP encode rolipram sensitive cAMP  
 XX  
 Sequence 498 AA;  
 SQ

Query Match 58.9%; Score 1419.5; DB 17; Length 498;  
 Best Local Similarity 61.7%; Pred. No. 2.5e-130; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERGETLFENDQNACKVCVCMGIDRLRQGTGVAERRSYPPIDFRLNSTYSGIK 66  
 DB 62 qrrgaisyddsdqtaiyimrlgdyvrrsragfeserrsgpypidfrifhsaeievvs 121  
 QY 67 KVKRKLISFORVFHSLRRLGIIPOAPLULDDYQARHMLSKYGMWDIFDRIT 126  
 DB 122 rrirrlsfqrylssrrfrtgatvnsnillddinggakcmlekygnwnidifdr 181  
 QY 127 NGNSLVLCLFLNPHGLKIDMVTHRFVYVMDYBDSQNPYHNAVADYQAMH 186  
 DB 182 ngslystlfhsinglleyfhcmklrlfimqyedynsqnpymhnaadtcqam 241  
 QY 187 CYLKEPLKASLTPUDIMIGLAAAHVDHPAVQNPQPLIKHNHLANLYNMSVLENHH 246  
 DB 242 cylkekplksavtpudimigllaaahdhpqnpqfiknhyatlyntsvylenh 301  
 QY 247 WRSTIGLMLRSLHLKPKEMTQDIEQGLSLIATDINRNEFLTRUKAHLNKDLR 306  
 DB 302 wrsavvllresgfsqfhsplresrqmetgqigallatodisrqheylsifrsldrgdcl 361  
 QY 307 DAQDRFLMOTIAKADICINPCRWEMSWRSRVCYFYGELKFELEISPLCNOQ 366  
 DB 362 dtrhrvlvilmalkcadicinpcrtwelskqwsckvtffagdiekyhgvspcldrn 421  
 QY 367 KDSPISIQGRMSYIYEPFREWHFTGNTSUSENMGHHLANKAOKWSLPRORSRS 426  
 DB 422 tesianiqigfimtlyvepitewarfs-ntrlsqtmighvglinkswkgq-greqssedt 480  
 QY 427 SG5 429  
 DB 481 daa 483  
 DR WPI; 1999-619709/53.  
 DR N-FSDB; AAT32240.  
 XX  
 PT New isolated RAS-related polypeptides and mammalian cyclic nucleotide  
 PT phosphodiesterases, used for screening for agents which can modify  
 PT complement or suppress genetic defects  
 XX  
 PS Claim 2; Column 85-88; 145pp; English.  
 XX  
 CC The present invention describes new isolated RAS-related polypeptides  
 CC and mammalian cyclic nucleotide phosphodiesterases (PDEs). RAS-related  
 CC polypeptides are capable of complementing a defective RAS function in  
 CC yeast. The products can be used for screening for agents which can  
 CC modify, complement or suppress a genetic defect in a biochemical  
 CC pathway in which cAMP participates, or in a biochemical pathway which  
 CC is controlled, directly or indirectly, by a RAS protein and other  
 CC proteins affecting cell growth and maintenance. Developing agents that  
 CC will selectively act upon PDEs is directed toward reproducing the  
 CC desirable effects of cyclic nucleotides, e.g. bronchodilation,  
 CC increased myocardial contractility, anti-inflammation, yet without  
 CC causing the undesirable effects, e.g. increased heart rate or enhanced  
 CC lipolysis. The products can also be used for therapeutic, diagnostic, prognostic  
 CC and prognostic uses. AAZ3229 to AAZ3285, and AAY49803 to AAY49830,  
 CC represent sequences used in the exemplification of the present  
 invention.  
 XX  
 Sequence 498 AA;  
 SQ

Query Match 58.9%; Score 1419.5; DB 20; Length 498;  
 Best Local Similarity 61.7%; Pred. No. 2.5e-130; Mismatches 91; Indels 1; Gaps 1;

QY 7 ERGETLFENDQNACKVCVCMGIDRLRQGTGVAERRSYPPIDFRLNSTYSGIK 66  
 DB 62 qrrgaisyddsdqtaiyimrlgdyvrrsragfeserrsgpypidfrifhsaeievvs 121  
 QY 67 KVKRKLISFORVFHSLRRLGIIPOAPLULDDYQARHMLSKYGMWDIFDRIT 126  
 DB 122 rrirrlsfqrylssrrfrtgatvnsnillddinggakcmlekygnwnidifdr 181  
 QY 127 NGNSLVLCLFLNPHGLKIDMVTHRFVYVMDYBDSQNPYHNAVADYQAMH 186

Db 182 ngnslsvsifhifslnglieyhdumkrirriviqdynsqnpyhnavaadvrqamh 241  
Qy 187 CYKEPKLASEFNPDLIMGLAAAHDDHGVNQPLIKNNHHIANLYONMSVLENH 246  
Db 242 cykepklausvwpdilsliaathdhdhgvnqpliktnhyatlykutsvlenth 301  
Qy 247 WNSTIGMRESULAHUPKEMTODIEOOLGSLATDINRONEFLTRIKAHHNKDIRLE 306  
Db 302 wrsavgliresqfshipsrqmetqigalilatdisrqpeylsfrshldrgdicle 361  
Qy 307 DAQDRHFMQALKCADICNPRIWEMSKOWSERVCEFYROGELEOKFELISPCLNQ 366  
Db 362 dtthrhlvlqmalckadicnpertweskqwekvteefhagdiekyhjgysplodrh 421  
Qy 367 KISIPSTQIGFMSYIVRPLFRWAHFTGNSLISENLGHANKAOWKSLIPRQHRSRG 426  
Db 422 tesianiqigfntlyliveplfetwarfs-ntrisqmlghvglnkaswkglgreqssedt 480  
Qy 427 SGS 429  
Db 481 daa 483

Search completed: September 13, 2002, 12:05:28  
Job time: 344 sec

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RX	MEDLINE-98007880; PubMed=9349724;	RA	Rena G., Begg F., Ross A., Mackenzie C., McPhee I., Campbell L.,
RA	Obernig R., Ratzliff J., Baecker P.A., Daniels D.V., Zuppan P.,	RA	
RA	Jarnagin K., Shelton E.R.,	RT	Houston E., Sullivan M., Housley M.D.,
RT	"Multiple splice variants of phosphodiesterase PDE4C cloned from human lung and testis."	RT	"Molecular cloning, genomic, promoter identification and
RT	Biochim Biophys Acta 1353:287-297 (1997).	RT	characterisation of the novel cAMP-specific phosphodiesterase,
RL	EMBL; U66346; ABAB6875_1;	RL	PDEA10.;"
DR	EMBL; U66347; AAB6876_1; -.	DR	Mol. Pharmacol. 0:0-0(2001).
DR	InterPro; IPR03607; Hoc.	DR	EMBL; AF110461; AAF14322.2; -.
DR	InterPro; IPR02073; PBase.	DR	InterPro; IPR03607; Hoc.
DR	Pfam; PF00233; PDEase; 1.	DR	Pfam; PF00336; PDEase; 1.
DR	PRINTS; PR00367; PDESTERASE1.	DR	PRINTS; PR00367; PDESTERASE1.
DR	SMART; SM00471; Hoc; 1.	DR	SMART; SM00471; Hoc; 1.
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Query Match	23.3%; Score 562; DB 4; Length 791; Best Local Similarity 28.2%; Pred. No. 6.3e-41; Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;	Query Match	23.3%; Score 562; DB 4; Length 791; Best Local Similarity 28.2%; Pred. No. 6.3e-41; Matches 137; Conservative 92; Mismatches 198; Indels 58; Gaps 10;
QY	11 EIEFENPDONAKCVCMLGDIRLRLRQGTGVRERAERGSYPPIDFRILN-----SITYSG-- 61	QY	11 EIEFENPDONAKCVCMLGDIRLRLRQGTGVRERAERGSYPPIDFRILN-----SITYSG-- 61
Db	283 KLAETLDELDWCDQDLETLQTHSGVGMASNEK-----RLNRETHLSTSRSQNO 336	Db	283 KLAETLDELDWCDQDLETLQTHSGVGMASNEK-----RLNRETHLSTSRSQNO 336
QY	62 -----EIGTRK-----KVKRRLSFQYFHASRLRLGTPQAPLHLDE 99	QY	62 -----EIGTRK-----KVKRRLSFQYFHASRLRLGTPQAPLHLDE 99
Db	337 VSEYISRFLDQTEVELPKVTAEEAPQPMRSRISGLHLGCHSASLSSATVPRGVQDQE 396	Db	337 VSEYISRFLDQTEVELPKVTAEEAPQPMRSRISGLHLGCHSASLSSATVPRGVQDQE 396
QY	100 DYLGQARHMLSKYGMMDDEFELDRLTNGNSVTLCHLFLNTIGLHFKLDFVTLHRLF 159	QY	100 DYLGQARHMLSKYGMMDDEFELDRLTNGNSVTLCHLFLNTIGLHFKLDFVTLHRLF 159
Db	397 EQLAKE--LEDTRNKGGLDVKYAEQLSGNQPLTAISIIFOERDLKTFQIPADTLATY 453	Db	397 EQLAKE--LEDTRNKGGLDVKYAEQLSGNQPLTAISIIFOERDLKTFQIPADTLATY 453
QY	160 VVQDVEYHQSNQPKINAVHAADVQAMHCLYKEPLAKSLTIPUDIMGLLAAAHWDVHPG 219	QY	160 VVQDVEYHQSNQPKINAVHAADVQAMHCLYKEPLAKSLTIPUDIMGLLAAAHWDVHPG 219
Db	454 LMLBGHYYHANVAYHNSLHAADVQATHVILLATPALEAVFTDLETAALFASATHDVHPIG 513	Db	454 LMLBGHYYHANVAYHNSLHAADVQATHVILLATPALEAVFTDLETAALFASATHDVHPIG 513
QY	220 VNPQFLIKTNHHLANLYQNSVLENHHRWSTIC3MRESR--LIAHLPKEMTQDIEQQLGS 277	QY	220 VNPQFLIKTNHHLANLYQNSVLENHHRWSTIC3MRESR--LIAHLPKEMTQDIEQQLGS 277
Db	514 VSNQFLINTNSEALMNYDASVLENHHLAVGFKLQQAENCDIQLNSAKORLSSLRMVYD 573	Db	514 VSNQFLINTNSEALMNYDASVLENHHLAVGFKLQQAENCDIQLNSAKORLSSLRMVYD 573
QY	278 LIDATDINQNEFTRLKAHLNKD-----LRLDAQDRHMLQALKCADICNCPCRW 331	QY	278 LIDATDINQNEFTRLKAHLNKD-----LRLDAQDRHMLQALKCADICNCPCRW 331
Db	574 MVALTDMSKHMNLADLKTIVETKVTSLGVLLDNYSDRIOVLYNQHCADLSNPTKPL 633	Db	574 MVALTDMSKHMNLADLKTIVETKVTSLGVLLDNYSDRIOVLYNQHCADLSNPTKPL 633
QY	332 EMSKQWSEERVICEYRQGELEQKFELESPLCNQKDSPSIQTIGFMSYIVELFREWAH 391	QY	332 EMSKQWSEERVICEYRQGELEQKFELESPLCNQKDSPSIQTIGFMSYIVELFREWAH 391
Db	634 PLYFQWTDTRIMAEFLFQGDRERSGLDITSPMCQKHTASYEVQSGFVLYAHLWETWAD 693	Db	634 PLYFQWTDTRIMAEFLFQGDRERSGLDITSPMCQKHTASYEVQSGFVLYAHLWETWAD 693
QY	392 FTGNTSLSENMGHLAHNKAQWKSLLPQRHRS RGSSGSGPDI-----DHAGQTESE 443	QY	392 FTGNTSLSENMGHLAHNKAQWKSLLPQRHRS RGSSGSGPDI-----DHAGQTESE 443
Db	694 LVHFD-----AQDLDTLEDREWYOSKIPRSPSDLTNPERGDPRDFQFELTLEEREEDEEE 751	Db	694 LVHFD-----AQDLDTLEDREWYOSKIPRSPSDLTNPERGDPRDFQFELTLEEREEDEEE 751
QY	444 EOBCD 448	QY	444 EOBCD 448
Db	752 EEEGE 756	Db	752 EEEGE 756
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Q9EQR7	PRELIMINARY; PRT; 771 AA.	Q9UPJ5	PRELIMINARY; PRT; 426 AA.
ID		ID	
AC		AC	
Q9EQR7;		Q9UJ5;	
DT	01-MAR-2001 (TREMBrel. 16, Created)	DT	01-MAY-2000 (TREMBrel. 13, Created)
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)	DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)	DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)
DE	CYCLIC AMP PHOSPHODIESTERASE PDE4A10 (FRAGMENT).	DE	PDE4C-426.
OS	Rattus norvegicus (Rat)	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurogauthi; Muridae; Murinae; Rattus.	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TAXID=1016;		NCBI_TAXID=9606;	
RN	[1]	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RP	Lamerdin J.E., McReady P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,

Search completed: September 13, 2002, 12:08:55  
Job time: 241 sec

## SUMMARIES

Searched: 283138 seqs, 96089334 residues

Chosen parameters for simulation

Minimum BB seq length: 6

Maximum Match 100%

卷之三

database

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2::  
pix2::*
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4 : Pir4 : \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## ALIGNMENTS

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2	1419.5	58.9	498	2	AA7286	3', 5' -cyclic-AMP
3	604.5	25.1	673	2	161358	3', 5' -cyclic-nuclei
4	603.5	25.1	584	2	B33109	3', 5' -cyclic-nuclei
5	603.5	25.1	672	2	161259	3', 5' -cyclic-nuclei
6	580.5	24.1	562	2	151143	CAMP phosphodiesterase
7	580.5	24.1	564	2	AA0949	cyclic-AMP phosphodiesterase
8	567.5	23.6	564	2	JC5159	3', 5' -cyclic-nuclei
9	567.5	23.6	736	2	161354	phosphodiesterase
10	565	23.5	886	2	A24442	3', 5' -cyclic-nuclei
11	559.5	23.2	610	2	167946	3', 5' -cyclic-nuclei
12	559.5	23.2	844	2	153865	phosphodiesterase
13	553	23.0	712	2	S11620	3', 5' -cyclic-nuclei
14	529.5	22.0	536	2	167945	3', 5' -cyclic-nuclei
15	517	21.5	549	2	TU6769	hypothetical protein
16	493	20.5	777	2	S65543	3', 5' -cyclic-nuclei
17	477.5	19.8	323	2	S55348	3', 5' -cyclic-nuclei
18	468	19.4	267	2	B33904	CAMP phosphodiesterase
19	468	19.4	535	1	A63378	3', 5' -cyclic-nuclei
20	467	19.4	534	1	A41162	3', 5' -cyclic-nuclei
21	466	19.4	519	2	T4783	hypothetical protein
22	466	19.4	535	1	A44161	3', 5' -cyclic-nuclei
23	461	19.1	664	2	T24549	hypothetical protein
24	454.5	18.9	530	1	AA5334	3', 5' -cyclic-nuclei
25	452.5	18.8	768	2	T10748	3', 5' -cyclic-nuclei
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27	445.5	18.5	713	2	JW0088	3', 5' -cyclic-nuclei
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29	409	17.0	491	2	A44283	3', 5' -cyclic-nuclei

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human  
 N| Alternative names: cAMP-specific phosphodiesterase 7B  
 C| Species: Homo sapiens (man)  
 C| Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 17-Nov-2000  
 C| Accession: JCT266  
 R| Sasaki, T.; Kotera, J.; Yuasa, K.; Oomori, K.  
 R| Biochem. Biophys. Res. Commun. 271, 575-583, 2000  
 A| Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.  
 A| Reference number: JCT266  
 A| Accession: JCT266  
 A| Molecule type: mRNA  
 A| Residues: 1-450 <SAS>  
 A| Cross-references: DDBJ:AB038040  
 A| Experimental source: caudate nucleus  
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 A| Gene: pde7B  
 A| Map position: 6q23-24  
 C| Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent  
 C| Keywords: phosphoric diester hydrolase

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C;Date: 03-May-1994	#sequence_revision 03-May-1994 #text_change 03-Nov-2000		
C;Accession: A47286			
R;Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodgers, J. Biol. Chem. 268, 12925-12932, 1993			
A;Title: Isolation and characterization of a previously undetected human cAMP phosphodiesterase			
A;Reference number: A47286; MUID:93286141			
A;Accession: A47286			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Cross-references: GR:L12052; NID:917992; PID:917983			
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Db	62	ORRGAISYDSDSOTALIIRMGDVYRVRSGAFESERRGSHPYIDPRIFHSQSELEVS	121
Qy	67	RKVKAISYFOSRPFYHARSLRQGIPAPLHLDLDEYLQGARHMLSKVGWMDPFLFR	126
Db	122	RNIRRLSFQYRLSRSEFFGTAWSNLNLDDYNGQAKCMLKVGWNNDPFLFR	181
Qy	127	NGNSLVLICLHLFNLNTHLHFKLUDMVTHFLRFLYMQEDYHSQNPYHNAVADTOAMH	186
Db	182	NGNSLVLICLHLFNLNTHLHFKLUDMVTHFLRFLYMQEDYHSQNPYHNAVADTOAMH	241
Qy	187	CYKLKRPLASFLTPLDMLGIGLLAAAHDVDPHGYNQNPFLKINHHLANLYQNSVLENHH	246
Db	242	CYLRKFPLAKNSVTPDILKSLAAATHDHLHFGVNPFLKTKHNTLYKNTSVLENHH	301
Qy	247	WRSTGMLBLAHLRPEKMTDIEODQLSLATDINRQEFTRLKAHLHNLKDLRE	306
Db	302	WRSAVGLRLRSGLLSPHLPLDERSQOMETOIGALIATADISRNQYELSLFRSHLDRGDLCE	361
Qy	307	DAQDRHFMQIQLAKCADTCNPCTRCWEMKQWSRVCBFPYRQGELEKQFEELISPQNO	366
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Qy	367	KDPSIQIGFMSTIVPLFREWAHTGNSTLSENMGHLAINKAQSKLPRQRHRSRG	426
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Qy	427	SGS 429	
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A;Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive			
C;Species: Homo sapiens (man)			
C;Date: 06-Sep-1996	#sequence_revision 06-Sep-1996 #text_change 17-Nov-2000		
C;Accession: I61358; I38416			
R;Bolega, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, J.			
RESULT	4		
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A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP-specific phosphodiesterases			
A;Reference number: A53109; MUID:94103234			
A;Accession: B53109			
A;Status: preliminary			
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A;Reference number: A53109; MUID:94103234			
A;Accession: B53109			
A;Status: preliminary			
A;Molecule type: DNA			
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A;Title: A family of human phosphodiesterases homologous to the duncle learning and memory protein			
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A;Molecule type: mRNA			
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A;Cross-references: GB:L20370; NID:9347129; PID:AAA03592.1; PID:9347130			
R;Becker, P.A.; Oberholter, R.; Bach, C.; Shelton, E.R.			
Gene 138, 252-256, 1994			
A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cAMP phosphodiesterase			
A;Reference number: I38416; MUID:94171048			
A;Accession: 138416			
A;Molecule type: mRNA			
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A;Cross-references: EMBL:002882; NID:9433346; PID:AAAC13745.1; PID:9433347			
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Qy	122	FDRLTNGNSLVLICLHLFNLNTHLHFKLUDMVTHFLRFLYMQEDYHSQNPYHNAVADTOAMH	180
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Qy	413	WKLSPRQRHRSRGSGSGPDIHDAGQTEEEQGDS	449
Db	572	YOSTIPO-----SPSPAPDPPBEGRCQTERQFELTLEEDGES	610

R; Swinnen, J. V.; Joseph, D. R.; Conti, M. Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989  
 A; Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormone  
 A; Reference number: A34414; MUID:90046763  
 A; Accession: A34414  
 A; Molecule type: mRNA  
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 A; Cross-references: GB:U09455; GB:M25349; NID:9517501; PID:AAA20401.1; PID:9517502; GB:  
 R; Swinnen, J.V.; Joseph, D.R.; Conti, M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989  
 A; Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP P  
 A; Reference number: GB:W05349  
 A; Accession: C33904  
 A; Status: preliminary  
 A; Molecule type: mRNA  
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 A; Status: preliminary; translated from GB/EMBL/DDBJ  
 A; Molecule type: mRNA  
 A; Residues: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 F; 237-465/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
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 Best Local Similarity 33.3%; Pred. No. 5e-40; Matches 135; Conservative 85; Mismatches 152; Indels 33; Gaps 9;  
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 Db 130 KEKKRPPMSQISGVKKLMISSLTSNCSIPRGVKEQDYLAKE---LEVNKGHLHVR 186  
 Qy 122 FDRLTNGSLVLTICH-LFNTGLHFLHFKDMLVHFLVWQEDYHSQNPYHVAHD 180  
 Db 187 IAEL-SGNRPLTVIHTIFQERDLKTFKIPVDTIYTLMLEDHYHADYVHNHHAAD 245  
 Qy 181 VTOAMHCYKLEPKLASFPLTDIMGLAAAHVDVHPGVNPQELIKTNHHLANLYQMS 240  
 Db 246 WQSTPHVLLSTPALEAVFTDLEILAAIFASA1HDVDPGVSNQFLINTSELALMNDSS 305  
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 C; Species: Rattus norvegicus (Norway rat)  
 C; Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 03-Nov-2000  
 C; Accession: 159143  
 R; Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989  
 A; Title: Isolation and characterization of a mammalian gene encoding a high-affinity  
 C; Accession: I61259; A53678; I67943  
 R; Sette, C.; Vicini, E.; Conti, M.  
 J. Biol. Chem. 269, 18271-18274, 1994  
 A; Title: The rat PDE5/IVd phosphodiesterase gene codes for multiple proteins differen  
 A; Reference number: A53678; MUID:94300405  
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 Qy 299 HNKD----LRLDAQDRHFLQALKCADICNPCCRIMWKMSKOMSERVCEEFYQGELE 352  
 Db 454 ETKKVTSQGVLLDNYSDRQVQLQNMVHCAADLSNTPKPLQYRQWTRIMEFFRQDRE 513  
 Qy 353 QKFELEISPICLNQQKDSIPISQIGMSYIYERLREWAHTGNTSLSENMLGHLAHNKAQ 412  
 Db 514 RERGMELSPMCDKHNASVEKSVQGFIDYIVHPLWETWADLVHFD--AQDILDTLEDNREW 571  
 Qy 413 WKSLLPQRHRSRGSSGSGPDHAGQGTSE-----EQEGDS 449  
 Db 572 YQSTIPQ-----SPSPAPDQEDGRQGQTEKFQFELTLEDEGES 610  
 RESULT 6  
 I59143  
 CAMP phosphodiesterase - rat (fragment)  
 C; Species: Rattus norvegicus (Norway rat)  
 C; Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 03-Nov-2000  
 C; Accession: 159143  
 R; Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989  
 A; Title: Isolation and characterization of a mammalian gene encoding a high-affinity  
 C; Accession: 159143; MUID:89264471  
 A; Reference number: 159143

Query Match 24 1%; Score 580.5; DB 2; Length 562; Best Local Similarity 31.9%; Pred. No. 3.2e-38; Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7; F; 231-459/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

QY 66 KKKVQLSLT---FORFYFASRLRGITPOAAPHLLRDPDYGQARHMLSKVGMWDFDIFL 121 Db 124 KKKQQLMTQISGVKLMHSSSLNNTSISRFGVNTENEDHLAKELDNLK--WGLNIFN 180

QY 122 FDLTNGLNSVLTLLCHLFNPHGLHFKLDMYLTHTLVMQEDYHSQNPYHNAADV 181 Db 181 VAGYSINRPLCIMAIQFQERDLKTFKISSDFTVITMLEDHYHSADVHNSLHAADV 240

QY 182 TQAMHCKLKEPKLASFLPLDIMGLLAAAHDDHGVNQPLKTHNLKLYNSV 241 Db 241 AOSTHVLSTLPALDAVFTOLEILAAIFAAAHDDHGVSNQFLINTNSLALMNDSEV 300

QY 242 LENHHRSTIGMLRBR---LLAHLPKENTODIEQOLQSLILATDINRQNEFLTRIKAHLH 299 Db 301 LENHHHLAVGKFLKQLEECDFQONITKKRQTRKVMWITDMLVATDKHMSLILLADTKMVE 360

QY 300 NRKD---LRLEDAQRDFMQLALKACDNCPCRWEMSKWOSERVICEBFYRGELEQ 353 Db 361 TTKVTSQGVLLDNYTDRQVLRNMYHCADLSNPKTSLKLYRQWTDRIMEFFQGDKER 420

QY 354 KFELETSPLCQOKQDPSIPIQIGMSVYVPEFREWAHTFGNSTLSENMGHLANKAW 413 Db 421 ERGMELSPMDKHTAVSVERKSQVGRIDYVHPLWETWADLVQPD- AODILDTLEDNRNNY 478

QY 414 KSLLPR----OHSRGSSGSGPDH--- AGOGTESERQEGDSP 450 Db 479 QSMIPOSPPPLDERSRDSQGQLMKFKPFEELTLEEDSESEGPEKEGEGP 525

RESULT 7

A0949 CYCLIC-AMP phosphodiesterase (EC 3.1.4.-) - rat N: Alternative names: PDE4/Jvb long form C: Species: Rattus norvegicus (Norway rat) C: Date: 13-May-1992 #text\_change 09-Jun-2000 C: Accession: A0949; D33904; A53109; 167942 J. Biol. Chem. 266, 18370-18377, 1991 A: Title: Properties and hormonal regulation of two structurally related cAMP phosphodiesterases A: Reference number: A40949; MUID:92011578 A: Accession: A0949 A: Status: preliminary A: Molecule type: mRNA A: Residues: 1-564 <SW1> A: Cross-references: GB:M25350 R. Swinnen, J.V.; Joseph, D.R.; Conti, M. Proc. Natl. Acad. Sci. U.S.A. 86, 5329-5329, 1989 A: Title: Molecular cloning of rat homologues of the Drosophila melanogaster *dunce* cAMP P: A: Reference number: A33904; MUID:89315790 A: Accession: D33904 A: Status: preliminary A: Molecule type: mRNA A: Residues: 210-476 <SW2> A: Cross-references: GB:M05350 R. Swinnen, J.V.; Joseph, D.R.; Conti, M. Proc. Natl. Acad. Sci. U.S.A. 86, 5329-5329, 1989 A: Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP P: A: Reference number: A53109; MUID:94103234 A: Accession: A53109 A: Status: preliminary A: Molecule type: DNA

Query Match 24 1%; Score 580.5; DB 2; Length 564; Best Local Similarity 31.9%; Pred. No. 3.2e-38; Matches 130; Conservative 91; Mismatches 159; Indels 27; Gaps 7; F; 233-461/Domain: 3', 5'-cyclic-nucleotide phosphodiesterase homology <CNP>

QY 66 KKKVQLSLT---FORFYFASRLRGITPOAAPHLLRDPDYGQARHMLSKVGMWDFDIFL 121 Db 125 KKKQQLMTQISGVKLMHSSSLNNTSISRFGVNTENEDHLAKELDNLK--WGLNIFN 182

QY 122 FDLTNGLNSVLTLLCHLFNPHGLHFKLDMYLTHTLVMQEDYHSQNPYHNAADV 181 Db 183 VAGYSINRPLCIMAIQFQERDLKTFKISSDFTVITMLEDHYHSADVHNSLHAADV 240

QY 182 TQAMHCKLKEPKLASFLPLDIMGLLAAAHDDHGVNQPLKTHNLKLYNSV 241 Db 243 AOSTHVLSTLPALDAVFTOLEILAAIFAAAHDDHGVSNQFLINTNSLALMNDSEV 302

QY 242 LENHHRSTIGMLRBR---LLAHLPKENTODIEQOLQSLILATDINRQNEFLTRIKAHLH 299 Db 303 LENHHHLAVGKFLKQLEECDFQONITKKRQTRKVMWITDMLVATDKHMSLILLADTKMVE 362

QY 300 NRKD---LRLEDAQRDFMQLALKACDNCPCRWEMSKWOSERVICEBFYRGELEQ 353 Db 363 TTKVTSQGVLLDNYTDRQVLRNMYHCADLSNPKTSLKLYRQWTDRIMEFFQGDKER 422

QY 354 KFELETSPLCQOKQDPSIPIQIGMSVYVPEFREWAHTFGNSTLSENMGHLANKAW 413 Db 423 ERGMELSPMDKHTAVSVERKSQVGRIDYVHPLWETWADLVQPD- AODILDTLEDNRNNY 480

QY 414 KSLLPR----OHSRGSSGSGPDH--- AGOGTESERQEGDSP 450 Db 481 QSMIPOSPPPLDERSRDSQGQLMKFKPFEELTLEEDSESEGPEKEGEGP 527

RESULT 8

JC1519 CYCLIC-AMP phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBPI06) C: Species: Homo sapiens (man) C: Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 21-Jul-2000 C: Accession: JC1519; A45500; 161359 R. Obernolte, R.; Brakha, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin Gene 129, 239-247, 1993 A: Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals A: Reference number: JC1519; MUID:93314968 A: Accession: JC1519 A: Molecule type: mRNA A: Residues: 1-564 <C0B> A: Cross-references: GB:112686 A: Experimental source: Lymphocyte A: Note: only partial nucleotide sequence is given R. McLaughlin, M.B.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P. J. Biol. Chem. 268, 6470-6476, 1993 A: Title: A low Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brain A: Reference number: A45500; MUID:93203241 A: Accession: A45500 A: Molecule type: mRNA A: Residues: 1-564 <MLC>

Query Match 23.6%; Score 567.5; DB 2; Length 564;  
 Best Local Similarity 31.3%; Pred No. 3.5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;  
 A; Accession: 161359  
 A; Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A; Residues: 1-564 <RES>  
 A; Cross-references: GB:120971; NID:9347131; PIDN:AAA03593.1; PID:9347132  
 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C; Keywords: phosphoric diester hydrolase  
 F; 423-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 564;  
 Best Local Similarity 31.3%; Pred No. 3.5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;  
 A; Accession: 161359  
 A; Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A; Residues: 1-564 <RES>  
 A; Cross-references: GB:120971; NID:9347131; PIDN:AAA03593.1; PID:9347132  
 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C; Keywords: phosphoric diester hydrolase  
 F; 423-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 564;  
 Best Local Similarity 31.3%; Pred No. 3.5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;  
 A; Accession: 161359  
 A; Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A; Residues: 1-564 <RES>  
 A; Cross-references: GB:120971; NID:9347131; PIDN:AAA03593.1; PID:9347132  
 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'  
 C; Keywords: phosphoric diester hydrolase  
 F; 423-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 564;  
 Best Local Similarity 31.3%; Pred No. 5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

RESULT 9  
 I61354  
 I; phosphodiesterase - human  
 C; Species: Homo sapiens (man)  
 C; Date: 20-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
 C; Accession: A54442; S55788; A36317; S55787  
 Q; LENHHRWSTIGMLRSR--LLAHIPKPEMTODEPOGLSITATINRONEFLTRKAHH 299  
 303 LENHHLAVSFKLQLQEHCDLIFMNLTKKORQTLRNMVDAVATOMSKHMSLLADLKTWE 362  
 Q; NKD-----LRLEDAQRDHFMQLTALKCADICNCPCRIWEMSKQNSRVICEEYRQELEQ 353  
 363 TKKVHSSGVLLDNTYDTRQVLRNNVHCADLSNPKSLYRQWDRTEEFFQGDKER 422  
 Q; RFELEISPLCQNQKQDSIPTSQIGMSYIPEPLFREWAHTGTNSTLSENMIGHAHNAKQW 413  
 423 ERGMELISPMDKHTASVEKSVQNGFIDYVHPLWETWADLWQPD-AQDILDTEDNRNWY 480  
 Q; KSLAPRQHRSRGSSGSGP----DHDAG-----QGTESEEGD 448  
 481 OSMTPO-----SPSPPLDEQNRDCQIGMKEFQPELTIDEDEDEGPEKEGE 525

RESULT 10  
 A54442  
 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splicing  
 N; Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A5 splice form  
 C; Species: Homo sapiens (man)  
 C; Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
 C; Accession: A54442; S55788; A36317; S55787  
 R; Bolger G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, B.; Mol. Cell. Biol. 13, 6558-6571, 1993  
 A; Title: A family of human phosphodiesterases homologous to the dunc learning and memory protein 1 2  
 A; Accession: A54442; MUID:94019330  
 A; Status: translated from GB/EMBL/DBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-886 <RES>  
 A; Cross-references: GB:120965; NID:9347119; PIDN:AAA03588.1; PID:9347120  
 R; Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.  
 Cell. Signal. 6, 793-812, 1994  
 A; Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a cAMP-specific phosphodiesterase 4A  
 A; Reference number: S55788; MUID:95194817  
 A; Accession: S55788  
 A; Molecule type: mRNA  
 A; Residues: 1-886 <RES>  
 A; Cross-references: EMBL:U18087; NID:9604374; PIDN:AAC50458.1; PID:9604375  
 C; Accession: 161354  
 R; Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs, B.; Mol. Cell. Biol. 13, 6558-6571, 1993  
 A; Title: A family of human phosphodiesterases homologous to the dunc learning and memory protein 1 2  
 A; Accession: A36317; MUID:90258854  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-886 <RES>  
 A; Cross-references: EMBL:U18087; NID:9604374; PIDN:AAC50458.1; PID:9604375  
 A; Note: 736-Ala was also found  
 R; Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Riggs, B.; Mol. Cell. Biol. 10, 2678-2686, 1990  
 A; Title: Cloning and expression of cDNA for a human low-K<sub>m</sub>, rolipram-sensitive cyclic nucleotide phosphodiesterase  
 A; Accession: A36317  
 A; Status: preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-886 <RES>  
 A; Cross-references: GB:M37744  
 C; Genetics:  
 A; Gene: GDB:DPDE2  
 A; Cross-references: GDB:138776; OMIM:600126  
 C; Map position: 19p13.1-19q12  
 C; Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
 F; 432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.6%; Score 567.5; DB 2; Length 736;  
 Best Local Similarity 31.3%; Pred No. 5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;

Query Match 23.6%; Score 567.5; DB 2; Length 886;  
 Best Local Similarity 31.3%; Pred No. 5e-37;  
 Matches 129; Conservative 93; Mismatches 149; Indels 41; Gaps 8;



Db	409 EDHYHADYAHNSHAADVQSLSTHVLATPALDAVFTDLEILALFAAIAHVDHPGVN	468	Db	318 EQLAKE--LEDINKWGLDVFKVADVGSGNRPLTAIFIQFQERDLKTFQIPADTLATYL	374
Qy	223 PFLIKTNHHLANLYNQMSYLENNHWRSTIGMIRESR - LLAHLPEKMQDIEQOLGSIL	280	Qy	160 VMQQEDYHSQNPYHNAVADYQAMHQLKEPLASTLTPIDMIGLAAAHVDHPVG	219
Db	469 QFLINTNSELALMYNDESVLENHHLAVGFKLQEQENCDFQNLSKRQRSLSRMMW	528	Db	375 LMLEGHYHANVAYHNSHAADVQSLSTHVLATPALAETFDLEILALFAAIAHVDHPVG	434
Qy	281 ATDINQRQEFILTRKALHNNKD-----LRLEDAQDRHFMQJALKCADICNPICRIMES	334	Qy	220 VNQPLIKTNHHLANLYQMSYLENNHWRSTIGMIRESR - LLAHLPEKMQDIEQOLGS	277
Db	529 ATDMSKHMLLADLQMTKVTYKTVTSSGVLLDNYSDTQVLRNNHVCADLSNPKPLY	588	Db	435 VSNQFLINTNSDVALMYNDAVSLENHHLAVGFKLQAOQNCDIFQNLSKRQSLRMMW	494
Qy	335 KQNSRVEEYFROGELQKFELEISPLCQNQKDSIPSTQIGMSYIVEPLFREWAHFTG	394	Qy	278 LILATDINQRQEFILTRKALHNNKD-----LRLEDAQDRHFMQJALKCADICNPICRIM	331
Db	589 RQWTDRIAMEFOODRERKRGMEISPAQDKHTRASVEKSQVGFIDYIVHPLWETWADLVH	648	Db	495 MVLATDMRSHMLLADLKVMVETKVTISGVLLDNYSDTQVLRNNHVCADLSNPKPL	554
Qy	395 NSTLSENMIGHLAHKNAQWSLLPROHRSRGSSGSGP - DHHDAGQG-----TE	441	Qy	332 EMSKQSEWSEVCEEYFQGELQKFELEISPLCQNQKDSIPSTQIGMSYIVEPLFREWAH	391
Db	649 PD-AQDILDTLEDNR-DW-----YHSIAQSPSPPLEEEPGGLGHPSLPLDKFQFELTL	699	Db	555 PLRYWTDRIAMEFOQGDREERESGLDSDPMCDKHTASVEKSQVGFIDYIAHPLWETWAD	614
Qy	442 SEROEGDS 449		Qy	392 FTGNSLSENMIGHLAHKNAQWSLLPROHRS RGSSSGPDH-----DHAGQFSE	443
Db	700 EEEFEEDS 707		Db	615 LVHED--AQDILDTLEDNREWYQSKIPSPSDLJNPERDGPDRQFELTEEEEEE	672
RESULT 13					
ST1626	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human				
N;Alternate names:	3',5'-cyclic AMP phosphodiesterase				
C;Species:	Homo sapiens (man)				
C;Date:	27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000				
C;Accession:	S71626; MUID:95145731				
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbeit, H.	FEBS Lett. 358, 305-310, 1995				
A;Title:	Molecular cloning and functional expression in yeast of a human cAMP-specific P				
A;Reference number:	S71626; MUID:95145731				
A;Accession:	S71626				
A;Molecule type:	DNA				
A;Residues:	1-712 <ENG>				
A;Cross-references:	EMBL:246632; PIDN:CAA86601.1; PID:9727223				
A;Experimental source:	substantia nigra				
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,	Mol. Cell. Biol. 13, 6558-6711, 1993				
A;Title:	A family of human phosphodiesterases homologous to the duncane learning and memory				
A;Reference number:	A54442; MUID:94019330				
A;Accession:	I61356				
A;status:	preliminary; translated from GB/EMBL/DBDJ				
A;Molecule type:	mRNA				
A;Residues:	462-712 <RES>				
A;Cross-references:	GB:127051; PIDN:941601; PIDN:AA56858.1; PID:9436012				
A;Gene:	HSPDE4C1				
C;Function:	A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP				
A;Pathway:	cyclic nucleotide metabolism				
A;Note:	expressed in various tissues but not in cells of the immune system				
C;superfamily:	3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'				
C;Keywords:	phosphoric diester hydrolase				
C;Cross-references:	GB:120968; PIDN:AAA03591.1; PID:9347126				
C;genetics:					
A;Molecule type:	mRNA				
A;Residues:	230-496 <SWI>				
A;Cross-references:	GB:M25347; GB:M28410				
C;Superfamily:	3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'				
C;Keywords:	alternative splicing; cAMP binding; phosphoric diester hydrolase				
F;253-481/Domain:	3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>				
Query Match	23.0%; Score 553; DB 2; Length 712;				
Best local Similarity	27.8%; Pred. No. 6.8e-36; Matches 135; Conservative 94; Mismatches 198; Indels 58; Gaps 10;				
Qy	11 EELFENPDPONAKVCMGLDIRLRLQGTYRAERGGSYFIDFLN-----SNTYSG--				
Db	204 KLAETLDBLWCDQDLETLQTRVSGEMASNPK-----RILNRETHLSENSRSQ				
Qy	62 -----EIGTRK-----KVKRLSFLQYFHASRLRLGIPQAPHLHIDE				
Db	258 VSEYISRTFLDQTEVEPLKVAEEAPQPMRISGLHGLCHASLSSATVPRFGVQDQE				
Qy	100 DYLQGQARHMLSKVQWMDDEFIDFLDRLTNQNSLVLCHLFNTLHIFKLDLAVTLHRL				
Db	700 EEEFEEDS 707				
Query Match	22.0%; Score 529.5; DB 2; Length 536;				
Best Local Similarity	30.8%; Pred. No. 3.4e-34; Matches 120; Conservative 79; Mismatches 169; Indels 21; Gaps 7;				
Qy	71 RLLSFLQYFHASRLRLGIPQAPHLHIDEYQKPLHLDLQGARHMLSKVQWMDDEFIDFLDRLTNQNS				
Db	156 QITGLRKSCHTS-LPTAIPPRFGVQDQEPLQELAKE--LEDINKWGLVFLVKAELSGRP				
Qy	131 LVTLICHLFNTLHIFKLDLAVTLHRLGIPQAPHLHIDEYQKPLHLDLQGARHMLSKVQWMDDEFIDFLDRLTNQNS				
Db	212 LTAVIYFLVQERDLKTFQIPADTLRLLTLEGHYSWAVYHNSHAADVQSLSTHVLATPALAETFDLEILALFAAIAHVDHPVG				
Qy	191 EPLKIAFLPUDLIMGLLAAAHVDHPVGQDPLKQHNNPQYKHNHLANLYQMSYVLSLNLHWRSTIGMIRESR - LLAHLPEKMQDIEQOLGSIL				
Db	272 TPALEAVFDTLEVIAAIFCAIAHVDHPVGQDPLKQHNNPQYKHNHLANLYQMSYVLSLNLHWRSTIGMIRESR - LLAHLPEKMQDIEQOLGSIL				

QY 251 IGMLRESR--LLAHLPKEMQDLEQQQLSILATDINRQEFLTRKAHLNKD---- 302  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 332 FKLLOGENDCIFONLSTKQKLSIRRMDVIMLDMSKRHSJLADLKTVMENKKVMSLGV 391  
 QY 303 LRLEQAQDRIFMQLALKADICNCPRICWEMSKQSERVICECEFYROGELQKFELISPL 362  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 392 LLLDRYSDRIQVQLQSLVHCAADLSNPALKPLPPLYKWTERRIMMAEFFQQDRERSGLIDSPM 451  
 QY 363 CNQORDSISIISIQGFM SYVEPFLFREWAHFTGNTLSENMLGHLAHNKAOKNSLIPRQHR 422  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 452 CDKHFASVSKSQVFDIVAHPLMWTADLVHD- AQELDLDLEDNREWVQSRVP--- 505  
 QY 423 SRGSSGSGDH-- DHAQGTEBEQED 448  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 506 CSPPHAIKGPDFRFKELTLEETEEFEED 534

RESULT 15

T16769 hypothetical protein R153.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jun-2000

R;Kister, J.

submitted to the EMBL Data Library, June 1995

C;Description: The sequence of *C. elegans* cosmid R153.

A;Reference number: 218573

A;Accession: T16769

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-549 <KR>

A;Cross-references: EMBL:U28729; NID:9861238; PID:9861239; PIDN:AAA6B292.1; CESP:R153.1

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:R153.1

A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, cainmodulin-dependent; 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 21.5%; Score 517; DB 2; Length 549;

Best Local Similarity 32.6%; Pred. No. 3 5e-33; Matches 114; Conservative 32.6%; Mismatches 72; Indels 140; Gaps 6;

QY 105 ARHMLSKVGMWDDIFDIFLDRLTNGNSLVTLLCHLFWNHGILHHFKIDMVLHREFLVMOC 164  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 216 AVHM-QRIDLWDPVKEPKDLSKNSLTVWFLSLQRNLKFTERHQSFLVTLNLH 274  
 QY 165 DYHSQNPYHNAVHADYTOQAMCYLKEPKLASFLPLDIMGLLAAAHDVHDHGCVNQPF 224  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 275 HYRN-NHYNFIHADYTAQSMVHLMSPLVTFLEVLAIAFGAVHDVHDHGFTNOY 333  
 QY 225 LIKINHHHLANLYQNMVLENNHWRSTIGMERS- LLALHPLKEMTQDDEQQQLSLLAT 282  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 334 LINSNNEALIMYNDVSLHLLAVAFKLQDNCDFLANLSRKQLQFRKIVDMVLT 393  
 QY 283 DIURQNEFLTRKAHLH---- NKDLRLEAQDRIFMLOIPLALKADICNCPRICWEMSK 336  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 394 DMSKHMISLADIKTMVBAKKVAGNNVTVLQDVKYNDKIQVLOSMIHLADLSNPTKPIEQQ 453  
 QY 337 WSERVICEFYRCGELKEPLTSPQNCQDSTISIQGFM SYVEPFLFREWAHFTGNS 396  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 454 WNRQIMREYWRQDGKKEKGELGLBLSPWMDGRGNTIKSOVFDIVAHPLMWTADLVPPD 513  
 QY 397 TISENMIGHLAMNAQKSLPRQHSRGSSGSDHKGOGTSEEO 446  
 QY :|: :|: :|: :|: :|: :|: :|: :|: :|:  
 Db 514 -AQTIDDQLEENREWVOSRIP----- EPDTARTVPEDEIK 549